

FIGURE 1

	gcggccgccc	ctgacacaat	ggctcagctt	atgcctcagc	gcagttcgc	ccaccccaga	60
5	atggcatcct	gcagaataca	cggcccctca	tcccatccc	gcgccagaga	caccggccag	120
	cccactgtcc	ccgccacaca	ttaaacttga	tcctcctaca	cagacgcact	cggagcagag	180
	cgcttataca	agcgcacagc	cgtctccggc	accgccacac	agacagatga	tgccgccccg	240
	accgacggcc	agccccagac	acaaccttct	gaaaacacag	aaaacaagtc	ccagcccaag	300
	cggctgcatg	tgtccaacat	ccccttcggg	ttccgggatc	cagacctccg	acaaatgttt	360
10	ggccaatttg	gtaaaatatt	agatgttgaa	attattttta	atgagcgggg	ctcgaaggga	420
	tttggtttcg	taactttcga	aaaatagtgcg	gatgcggaca	gggcgaggga	gaaattgcac	480
	ggtaccgtgg	tagagggccg	taaaatcgag	gttaataatg	cgacagcacg	cgtg atg	537
					Met		
					1		
15	act aat aaa aag gcc gtg aac ccc tac acc aat ggc tgg aaa tta aat	585					
	Thr Asn Lys Lys Ala Val Asn Pro Tyr Thr Asn Gly Trp Lys Leu Asn						
	5 10 15						
20	cca gtt gtg ggc gcg gtc tac agc ccc gac ttc tat gca ggc acg gtg	633					
	Pro Val Val Gly Ala Val Tyr Ser Pro Asp Phe Tyr Ala Gly Thr Val						
	20 25 30						
25	ctg ttg tgc cag gcc aac cag gag gga tct tcc atg tac agt ggc ccc	681					
	Leu Leu Cys Gln Ala Asn Gln Glu Gly Ser Ser Met Tyr Ser Gly Pro						
	35 40 45						
30	agt tca ctt gta tat act tct gca atg cct ggc ttt cca tat ccg gcc	729					
	Ser Ser Leu Val Tyr Thr Ser Ala Met Pro Gly Phe Pro Tyr Pro Ala						
	50 55 60 65						
35	gcc act gct gca gct gca tac cga ggg gct cac ctt cga ggc cgt ggt	777					
	Ala Thr Ala Ala Ala Ala Tyr Arg Gly Ala His Leu Arg Gly Arg Gly						
	70 75 80						
40	cgc acc gtg tac aac acc ttc aga gct gcg gcg ccc cca ccc cca atc	825					
	Arg Thr Val Tyr Asn Thr Phe Arg Ala Ala Ala Pro Pro Pro Pro Ile						
	85 90 95						
45	ccg gcc tat ggc gga gta gtg tat caa gag cca gtg tat ggc aat aaa	873					
	Pro Ala Tyr Gly Gly Val Val Tyr Gln Glu Pro Val Tyr Gly Asn Lys						
	100 105 110						
50	ttg cta cag ggt ggt tac gct gca tac cgc tac gcc cag ccc acc cct	921					
	Leu Leu Gln Gly Gly Tyr Ala Ala Tyr Arg Tyr Ala Gln Pro Thr Pro						
	115 120 125						
55	gcc act gct gct gcc tac agt gac agt tac gga cga gtt tat gct gcc	969					
	Ala Thr Ala Ala Ala Tyr Ser Asp Ser Tyr Gly Arg Val Tyr Ala Ala						
	130 135 140 145						
60	gac ccc tac cac cac aca ctt gct cca gcc ccc acc tac ggc gtt ggt	1017					
	Asp Pro Tyr His His Thr Leu Ala Pro Ala Pro Thr Tyr Gly Val Gly						
	150 155 160						
65	gcc atg aat gct ttt gcg ccc ttg acc gat gcc aag act agg agc cat	1065					

FIGURE 1 (cont.)

5	Ala Met Asn Ala Phe Ala Pro Leu Thr Asp Ala Lys Thr Arg Ser His	
	165 170 175	
	gct gat gat gtg ggt ctc gtt ctt tct tca ttg cag gct agt ata tac	1113
10	Ala Asp Asp Val Gly Leu Val Leu Ser Ser Leu Gln Ala Ser Ile Tyr	
	180 185 190	
	caa ggg gga tac aac cgt ttt gct cca tat taaatgataa aaccattaaa	1163
	Gln Gly Gly Tyr Asn Arg Phe Ala Pro Tyr	
	195 200	
15	caaacaagca aaaaacaaaa caaaaacaaa aaaaccaacc ttccaatgtg gggagagagg	1223
	aagctttccg aggcccgagt gttcgacac atgcagtagg acatcacttt agcaactcaa	1283
	agaaacaacg aaaaaaaaaa aaaaaaaaaa aataagcggc cgaaggggtt cgctaga	1340
20		
25		
30		
35		
40		
45		
50		
55		

FIGURE 2

5	tctagcgaac cccttcgcga aggggttcgc ctgtgctggt gggcgcggtg gcccgaagcc	60
	ttggactcac tgcaggactg tgcagggaac cactgtccaa gcatcgggct aatagggggc	120
	gcctgcctcg gtttaccctt cagcgtctgg tgaaatcccc cagcgtctag ggaaagatcc	180
	gttctgctcc gcgaggggaaa cagagccgtt gacc atg gtt gca acg ggc agt ttg	235
	Met Val Ala Thr Gly Ser Leu	
10	1 5	
	agc agt aag aac acg gcc agc att tca gag ttg ctg gac ggt ggc tct	283
	Ser Ser Lys Asn Thr Ala Ser Ile Ser Glu Leu Leu Asp Gly Gly Ser	
	10 15 20	
15	cac cct ggg agt ctg cta agt gat ttc gac tac tgg gat tat gtc gtc	331
	His Pro Gly Ser Leu Leu Ser Asp Phe Asp Tyr Trp Asp Tyr Val Val	
	25 30 35	
20	cct gag ccc aac ctc aac gag gtg gtg ttt gaa gag aca aca tgc cag	379
	Pro Glu Pro Asn Leu Asn Glu Val Val Phe Glu Glu Thr Thr Cys Gln	
	40 45 50 55	
	aat ttg gtt aaa atg ttg gag aac tgt ctg tcc aag tca aag caa acc	427
25	Asn Leu Val Lys Met Leu Glu Asn Cys Leu Ser Lys Ser Lys Gln Thr	
	60 65 70	
	aaa ctc ggt tgc tct aag gtc ctg gtt cct gag aaa ctg acc cag aga	475
	Lys Leu Gly Cys Ser Lys Val Leu Val Pro Glu Lys Leu Thr Gln Arg	
30	75 80 85	
	att gcc caa gat gtc ctg cgg ctc tca tcc aca gag ccc tgc ggc ctt	523
	Ile Ala Gln Asp Val Leu Arg Leu Ser Ser Thr Glu Pro Cys Gly Leu	
	90 95 100	
35	cgg ggc tgt gtt atg cac gtg aac ttg gaa att gaa aat gtg tgt aaa	571
	Arg Gly Cys Val Met His Val Asn Leu Glu Ile Glu Asn Val Cys Lys	
	105 110 115	
40	aag ctg gat agg att gtg tgt gat gct agt gtg gtg ccg acc ttt gag	619
	Lys Leu Asp Arg Ile Val Cys Asp Ala Ser Val Val Pro Thr Phe Glu	
	120 125 130 135	
	ctc acg ctg gtg ttc aag cag gag agc tgc tcc tgg acc agc ctc aag	667
45	Leu Thr Leu Val Phe Lys Gln Glu Ser Cys Ser Trp Thr Ser Leu Lys	
	140 145 150	
	gac ttc ttc ttt agc gga ggt cgc ttc tcg tcg ggc ctt aag cga act	715
	Asp Phe Phe Phe Ser Gly Gly Arg Phe Ser Ser Gly Leu Lys Arg Thr	
50	155 160 165	
	ctg atc ctc agc tcg gga ttt cga ctt gtt aag aaa aaa ctg tac tct	763
	Leu Ile Leu Ser Ser Gly Phe Arg Leu Val Lys Lys Lys Leu Tyr Ser	
	170 175 180	
55	ctg att gga acg aca gtc att gag gag tgc tga ggaggaaaaa acaattaaag	816
	Leu Ile Gly Thr Thr Val Ile Glu Glu Cys *	

Sequence

190

FIGURE 2 (cont.)

867

10

15

20

25

30

35

40

45

50

55

FIGURE 3

5	tctagcgaac cccttcggtg gacagaacag cctgagtcag g atg aaa gct ctc agg	56
	Met Lys Ala Leu Arg	
	1 5	
10	gct gtc ctc ctg atc ttg cta ctc agt gga cag cca ggg agc agc tgg	104
	Ala Val Leu Leu Ile Leu Leu Leu Ser Gly Gln Pro Gly Ser Ser Trp	
	10 15 20	
15	gca caa gaa gct ggc gat gtg gac ctg gag cta gag cgc tac agc tac	152
	Ala Gln Glu Ala Gly Asp Val Asp Leu Glu Leu Glu Arg Tyr Ser Tyr	
	25 30 35	
20	gat gat gac ggt gat gac gat gat gac gat gat gaa gaa gag gaa gag	200
	Asp Asp Asp Gly Asp Asp Asp Asp Asp Asp Asp Glu Glu Glu Glu Glu	
	40 45 50	
25	gag gag acc aac atg atc cct ggc agc agg gac aga gca ccg cct cta	248
	Glu Glu Thr Asn Met Ile Pro Gly Ser Arg Asp Arg Ala Pro Pro Leu	
	55 60 65	
30	cag tgc tac ttc tgc caa gtg ctt cac agc ggg gag agc tgc aac gag	296
	Gln Cys Tyr Phe Cys Gln Val Leu His Ser Gly Glu Ser Cys Asn Glu	
	70 75 80 85	
35	aca cag aga tgc tcc agc agc aag ccc ttc tgt atc aca gtc atc tcc	344
	Thr Gln Arg Cys Ser Ser Ser Lys Pro Phe Cys Ile Thr Val Ile Ser	
	90 95 100	
40	cat ggc aaa act gac aca ggt gtc ctg acg acc tac tcc atg tgg tgt	392
	His Gly Lys Thr Asp Thr Gly Val Leu Thr Thr Tyr Ser Met Trp Cys	
	105 110 115	
45	act gat acc tgc cag ccc atc gtg aag aca gtg gac agc acc caa atg	440
	Thr Asp Thr Cys Gln Pro Ile Val Lys Thr Val Asp Ser Thr Gln Met	
	120 125 130	
50	acc cag acc tgt tgc cag tcc aca ctc tgc aat att cca ccc tgg cag	488
	Thr Gln Thr Cys Cys Gln Ser Thr Leu Cys Asn Ile Pro Pro Trp Gln	
	135 140 145	
55	agc ccc caa atc cac aac cct ctg ggt ggc cgg gca gac agc ccc ttg	536
	Ser Pro Gln Ile His Asn Pro Leu Gly Gly Arg Ala Asp Ser Pro Leu	
	150 155 160 165	
60	aag ggt ggg acc aga cat cct caa ggt gac agg ttt agc cac ccc cag	584
	Lys Gly Gly Thr Arg His Pro Gln Gly Asp Arg Phe Ser His Pro Gln	
	170 175 180	
65	gtt gtc aag gtt act cat cct cag agt gat ggg gct cac ttg tct aag	632
	Val Val Lys Val Thr His Pro Gln Ser Asp Gly Ala His Leu Ser Lys	
	185 190 195	
70	ggg ggc aag gct aac cag ccc cag gga aat ggg gcc gga ttc cct gca	680

FIGURE 3 (cont.)

5	Gly Gly Lys Ala Asn Gln Pro Gln Gly Asn Gly Ala Gly Phe Pro Ala	
	200 205 210	
	ggc tgg agc aaa ttt ggt aac gta gtt ctc ctg ctc acc ttc ctc acc	728
10	Gly Trp Ser Lys Phe Gly Asn Val Val Leu Leu Leu Thr Phe Leu Thr	
	215 220 225	
	agt ctg tgg gca tca ggg gcc taa agactcgtcc tcccccaacc aggacccttc	782
	Ser Leu Trp Ala Ser Gly Ala *	
15	230 235	
	agcctttcct ccctgacaac cagcttcaga gaataaactt gaatgtcttt tgccatctaa	842
	aaaaaaaaa aaaaaaaaaa aaagcggccg cc	874
20		
25		
30		
35		
40		
45		
50		
55		

FIGURE 4

5	tctagcgaac cccttcgagc gaaccccttc ggccagtacc ctgagccctg gtcctcctctg	60
	gagctgcccc acagctctga ctgtggactg agggatgtta ggcggatcac ctgagcctcc	120
	agaggctcac acta atg agc ggg cgc tct ctt ctt agc cac tgt tgc att	170
	Met Ser Gly Arg Ser Leu Leu Ser His Cys Cys Ile	
	1 5 10	
10	tgg ttt tca ttg act cct ggg cct cgt ttg agt gac act gtc ctt gtc	218
	Trp Phe Ser Leu Thr Pro Gly Pro Arg Leu Ser Asp Thr Val Leu Val	
	15 20 25	
15	ttt tgt ttc aga gct ctc cca gtg tta gtg gac tca gat gag gaa att	266
	Phe Cys Phe Arg Ala Leu Pro Val Leu Val Asp Ser Asp Glu Glu Ile	
	30 35 40	
20	atg acc aga tct gaa ata gct gaa aaa atg ttc tct tca gaa aag ata	314
	Met Thr Arg Ser Glu Ile Ala Glu Lys Met Phe Ser Ser Glu Lys Ile	
	45 50 55 60	
25	atg tga tcagggcccc agtgggtcca gtgtgcatgg gagcgcggtc aggtgatggg	370
	Met *	
30	aaaggcctgg ctctcgtcaa aactgacagc tgcgctatga tacatgtctc actttgtttgt	430
	cttggagatc tgtgtatgca ggtgaagaac tcaagtgtgg gaggggtctgc cgcctcagaa	490
	agccatcttt gaaacggact cataaagtca gttttgtttgc cattaagttg cctgattttg	550
	gaaacaattt aagaagtgtt aaagacatgt gttcagatgc ctcttaggcg gcagccacag	610
	gcatgccagg ttgtgtccct cagttttctc cagacaaaag aatctgcagc tgggcgtggc	670
	ggcacactac tggcagttga aagtctgtaa tttcaaggcc aagcctggtc tacatagttc	730
	caggacaacc agagagatct acatagttag accctgcctc aaaacacaga aaccnnanna	790
	naaaaaaaaaa aaaaaaaaaaag cggccgc	817
35		
40		
45		
50		
55		

FIGURE 5

5	tctagcgaac cccttcgcac atgggttcct gctgaccaag gggacatggc tctgaagatg	60
	atgaggctgg ttactcagca ggagtagctg agctgagctg gccctggagg ccctggaggc	120
	cctggagtag ggcccagg atg cag gtg cta atg tct atc ccc ggc gct ctt	171
	Met Gln Val Leu Met Ser Ile Pro Gly Ala Leu	
	1 5 10	
10	ctt ccc gac tct acc atg gga tgt aac tcc agg agc ccc tgc cat ctc	219
	Leu Pro Asp Ser Thr Met Gly Cys Asn Ser Arg Ser Pro Cys His Leu	
	15 20 25	
15	ccg tac caa aag act gtg gct tcc gtg tct act cag aaa tca gtt cta	267
	Pro Tyr Gln Lys Thr Val Ala Ser Val Ser Thr Gln Lys Ser Val Leu	
	30 35 40	
20	ctt cgt aaa cag tgt tta aaa cca gac tca ttt aat cag agt gaa gga	315
	Leu Arg Lys Gln Cys Leu Lys Pro Asp Ser Phe Asn Gln Ser Glu Gly	
	45 50 55	
25	ttg cag tcc att ggc ttc tta gca cag aag cag ctg ata aca caa gta	363
	Leu Gln Ser Ile Gly Phe Leu Ala Gln Lys Gln Leu Ile Thr Gln Val	
	60 65 70 75	
	aac ccc agc cct tga gaggtagaag caagaggatc agaggttcaa gcgcatacctc	418
	Asn Pro Ser Pro *	
30	ggctccatca caagttcaaaa agccgcctgc accaaatggg agtccttgct tcaaaaaaaaa	478
	aaaaaaaaaa agcaaagaaa gcaaaggact cgatgacatg atttatagac aaaagcagtg	538
	ggagaaaaata ctaaaagcccc actgagctgc cagccagggtg tctgtgacta caggtctttt	598
	atctgctcat atatattttt acaaaaaaatg aaattcatat tggtcgctat tttgctggct	658
35	gctttgctcc cgatcaacat gatttgcacg ttttttccat caataaatgt gccatgatat	718
	ttttaaaaaa aaaaaaaaaa aaaaaaaaaa gggcncc	755
40		
45		
50		
55		

FIGURE 6

5	tctagcgaac cccttcgcag ctctctgacc tgcgtcgccg ccgctctccg ctcttgattt	60
	cgccgtg atg tcg acc gca atg aac ttc ggg acc aaa agc ttc cag ccg	109
	Met Ser Thr Ala Met Asn Phe Gly Thr Lys Ser Phe Gln Pro	
	1 5 10	
10	cgg ccc cca gac aaa ggc agc ttc ccg cta gac cac ttc ggt gag tgt	157
	Arg Pro Pro Asp Lys Gly Ser Phe Pro Leu Asp His Phe Gly Glu Cys	
	15 20 25 30	
15	aaa agc ttt aag gaa aaa ttc atg aag tgt ctc cgc gac aag aac tat	205
	Lys Ser Phe Lys Glu Lys Phe Met Lys Cys Leu Arg Asp Lys Asn Tyr	
	35 40 45	
20	gaa aat gct ctg tgc aga aat gaa tct aaa gag tat tta atg tgc agg	253
	Glu Asn Ala Leu Cys Arg Asn Glu Ser Lys Glu Tyr Leu Met Cys Arg	
	50 55 60	
25	atg caa agg cag ctg atg gca cca gaa cca cta gag aaa ctc ggc ttt	301
	Met Gln Arg Gln Leu Met Ala Pro Glu Pro Leu Glu Lys Leu Gly Phe	
	65 70 75	
30	aga gac ata atg gag gag aaa ccg gag gca aag gac aaa tgt tga	346
	Arg Asp Ile Met Glu Glu Lys Pro Glu Ala Lys Asp Lys Cys *	
	80 85 90	
35	gaatcactgg gctgtgtccc cctacctgga gcagagctga gcccttctgc ccaccgtgga	406
	gagagctgag ccatacctgtg ctgcccagag gaggggctct ccgtgtcgac tttggctcat	466
	ccctgcagca cagaccaaac tgctttctct actgaccaca cttctgcttc agagagnggt	526
	ttctcctgtc tgngtgtggc acaggatctg ctcanggctg aacactgatg tgatatgata	586
	tcccacctag tgtggccgca caccaaaaagg cctggacagg atttcacagt gactcaacct	646
	gagtcctcac acccggaacc tgtcagcgaa aaccaancga agcaaaatgn ctggcttttg	706
	gcttacaaac cccatnattt gntttccctt ctcttgggtc tttgttttga caaanctggc	766
	atacaaagtn ggaaggggga aataaaaaaa aaaaaaaaaa	806
40		
45		
50		
55		

FIGURE 7

5	tctagcgaac cccttcncga aggggttcgc cgagaggtgg gagccaaaag gatggagcat	60
	ccgccggtgg tggctggtgg ccgcaatctt ggtggtcctg atcgggggttg tcttagtctg	120
	cctgatagtc tacttcgcca acgcagcgcga cagcgaggcc tgtaagaacg ggttgcggtt	180
	gcaggatgag tgccgaaaca ccacgcacct gttgaagcac cagctnaccg gcgcccagga	240
	cagcctgctg cagacggag atg cag gca aac tcc tgc aac cag acc gtg atg	292
10	Met Gln Ala Asn Ser Cys Asn Gln Thr Val Met	
	1 5 10	
	gac ctt cgg gat tcc ctg aag aag aag gtg tct naa acc cag gag caa	340
	Asp Leu Arg Asp Ser Leu Lys Lys Val Ser Xaa Thr Gln Glu Gln	
15	15 20 25	
	can gcc cgc atc aag gaa ctt gag aat aag atc gag agg ctg aac caa	388
	Xaa Ala Arg Ile Lys Glu Leu Glu Asn Lys Ile Glu Arg Leu Asn Gln	
	30 35 40	
20		
	gag ctg gag aaa ttt gag gac cca aaa gga aat ttc tac cac agt gca	436
	Glu Leu Glu Lys Phe Glu Asp Pro Lys Gly Asn Phe Tyr His Ser Ala	
	45 50 55	
25		
	ngt gaa ctc aag cgg gtt cgt ggt ggn ctt can cct act tgt gct ttg	484
	Xaa Glu Leu Lys Arg Val Arg Gly Gly Leu Xaa Pro Thr Cys Ala Leu	
	60 65 70 75	
30		
	tgg cgg gac tgt tct nca ctt ttt ang acc caa taa ttgggangta	530
	Trp Arg Asp Cys Ser Xaa Leu Phe Xaa Thr Gln *	
	80 85	
35		
	caaacctgtg taggcattgn nggtngtaat ggcttttgag ggggtcctgg cacccttaag	590
	atgtgaanac cattangnng gacccaaaat gnnttttctt gntttgaact gggcgaggacc	650
	cggagtgggg ggcnggaaat aanntattnn ggnnggaaan aaaaaaaaaa aaaaaaaaaa	710
	gcggccc	717

40

45

50

55

FIGURE 8

5	tctagcgaac cccttcgccc agctgctaga agccaggctg gcctgggtgag gc atg agc	58
	Met Ser	
	1	
10	atg aag atg aac cca ggt gac aag gac aag atg ttg ctc ttc tcc cca	106
	Met Lys Met Asn Pro Gly Asp Lys Asp Lys Met Leu Leu Phe Ser Pro	
	5 10 15	
15	ccc ttt gac ccc tgt ctt cta agg cat cta gga agg aac cag tgt cct	154
	Pro Phe Asp Pro Cys Leu Leu Arg His Leu Gly Arg Asn Gln Cys Pro	
	20 25 30	
	tgg tac tga ttactttaga ttcaacctaa gggccagcc actgactaag	203
	Trp Tyr *	
	35	
20	gccaaggcca tttttccata cctggggaggg tagagattca gggttgtggg taagtgggca	263
	ctaaacatgg atttgcaagg gaaaacgaca gggcatcgag cttaaatttga atttacatga	323
	aattctgaaa tgtacttgta tgaagaaact gttatctgaa acctaactta aatgggcatc	383
	ctgccttttg tctgggtgaga aatgaaagtg atctacaata agtgtcaaag caacaaggcc	443
25	cctctggata tgtctaggcc aggatgagga tactaagtgc cttcaaagcg agagggaggc	503
	aggccaagaa cactgcccta ctgaaaggca ggcttggccg gctagggcct ccaaggccct	563
	gatccctgag gcaccacagc cacaacttgt gtaggcctgg cccaggtcag tgaataggtt	623
	ctaggcagtg gttctcaacc ttctaatgc tgcaaccctt caatacagtt tctcctgttg	683
	tagtaatccc caaccataaa attattttca ttgcgacttc ataactggac ttttgctact	743
30	gttatgaatc ataatgtaaa tatttttttg agctagaggt ttaccaaggg ggttgtgagc	803
	cataggttga aaaccattgt tctaggaata gctccagggg tggtttctga ggcccccgca	863
	aggtgggatc tatggggcag ggttgatct tctccaagag cccccaacag gatatatata	923
	tatatatata tatatatata tatatatata tactttgata gcatcccatg	983
	gaacgactgt ctctgatac taaagggagc ttggaagaaa ccaaggctga gagaagttgt	1043
35	agagtgggaa ggtaggcgaa gggattgagg tgacacagtg atagcccctt caggggtggg	1103
	tctaccnag acagcagata aaggccttag gatgggagat tactctggct gctcagagg	1163
	gaacacaggg acacagcacc aataaaatct ctttcttttc aaaaaaaaaa aaaaaaaaaa	1223
	aaaaagcggn cc	1235
40		
45		
50		
55		

FIGURE 9

5	tctagcgaac	cccttcgatt	ttattagctc	ttgcttctcc	attcctcata	atztatgaat	60
	tatacagcct	tcgcttgaat	acgcgtctga	agttatgctt	tgtgttggtg	tgggtttttt	120
	tttttttttc	ttttcttttt	ttttggagct	ggggaccgaa	cccagggcct	tgttgctcta	180
	ccactgagct	aaatccccaa	cccctgttgt	gtgttttaaa	taagtctctt	actgtccatt	240
	ttgtaattag	tgttgttacc	ttgtaataat	agacatcata	caaagtttcc	tcttttttgt	300
10	gccagtgctg	agaacatgag	aaacatttaa	tgagtatttg	tttgttaaat	aatatttata	360
	acggctagaa	tggcagacac	ac atg gta	gca cat gat	ggt gat ttt	cgg ggg	412
			Met Val	Ala His	Asp Gly	Asp Phe Arg Gly	
			1	5		10	

15	cct ttt gtt tgc tca gag ctg gta atc tct gcc ggt tgg ttt gct ttg	460
	Pro Phe Val Cys Ser Glu Leu Val Ile Ser Ala Gly Trp Phe Ala Leu	
	15 20 25	

20	cct ggt ctg gga cta acc tca cat ttt ctc act ctt gct ttc cga gag	508
	Pro Gly Leu Gly Leu Thr Ser His Phe Leu Thr Leu Ala Phe Arg Glu	
	30 35 40	

25	att agt cat cct tcc tgt cct act ggg ctc tcg ata gcg ctc atc agc	556
	Ile Ser His Pro Ser Cys Pro Thr Gly Leu Ser Ile Ala Leu Ile Ser	
	45 50 55	

30	ata ctg cat ttc aat ccc agc gaa ggg gtt cgc cga agg ggt tcg cta	604
	Ile Leu His Phe Asn Pro Ser Glu Gly Val Arg Arg Arg Gly Ser Leu	
	60 65 70	

35	ggc cag tgt gat gga tat ctg cag aat tc	633
	Gly Gln Cys Asp Gly Tyr Leu Gln Asn	
	75 80	

35

40

45

50

55

FIGURE 10

5	tctagcgaac cccttcgcct ttctccaaag ccttcccgtt tcctcttgac agctacgggc	60
	tgaggcagcc attcctgcag cagcgctcgg ccggtgaagg gccgaactga cgcttcctag	120
	atctgtctcg gctgaattac tctcacccgt ttccattctg tgtgcaccag aaatctgaga	180
	tccaggagta tcaacagcaa ag atg tct aat gag cca ccc cct cct tat cca	232
	Met Ser Asn Glu Pro Pro Pro Pro Tyr Pro	
10	1 5 10	
	gga ggg cct aca gcc cca cta ctg gag gaa aaa agt gga gcc cca cat	280
	Gly Gly Pro Thr Ala Pro Leu Leu Glu Glu Lys Ser Gly Ala Pro His	
	15 20 25	
15	acc cca ggc cga acc ttt cca gct gtg atg cag cca cca cca ggc atg	328
	Thr Pro Gly Arg Thr Phe Pro Ala Val Met Gln Pro Pro Pro Gly Met	
	30 35 40	
20	cca ctg ccc tct gtt gac att gcc ccc ccg ccc tat gag ccg cct ggc	376
	Pro Leu Pro Ser Val Asp Ile Ala Pro Pro Pro Tyr Glu Pro Pro Gly	
	45 50 55	
	cat cca ggg cct aag cct ggt ttw atg ccc ccc acn tta cca cac att	424
25	His Pro Gly Pro Lys Pro Gly Xaa Met Pro Pro Thr Leu Pro His Ile	
	60 65 70	
	cna ana acc ttn ntn tgt aaa agt taa ataanaangg agggattcga	471
	Xaa Xaa Thr Xaa Xaa Cys Lys Ser *	
30	75 80	
	nccccctnca acnggtttca agccaattty mtaaccattt tgtttttttc wtttaaaaaa	531
	aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggaaaaaaaa aaaaaaaaaa	591
	aaaaaagggg ggcccc	607
35		
40		
45		
50		
55		

FIGURE 11

5	tctagcgaac cccttcgcaa agtcctaagc cttac atg aga aaa ttt aag aca	53
	Mét Arg Lys Phe Lys Thr	
	1 5	
10	ccc tta atg att gcg gaa gaa aaa tac aga caa caa agg gaa gag ctt	101
	Pro Leu Met Ile Ala Glu Glu Lys Tyr Arg Gln Gln Arg Glu Glu Leu	
	10 15 20	
15	gag aaa cag aga cgg gag agt tct tgc cat agc atc atc aaa aca gaa	149
	Glu Lys Gln Arg Arg Glu Ser Ser Cys His Ser Ile Ile Lys Thr Glu	
	25 30 35	
20	acc cag cac cgc agc tta tca gag aaa gag aaa gaa aca gag tta caa	197
	Thr Gln His Arg Ser Leu Ser Glu Lys Glu Lys Glu Thr Glu Leu Gln	
	40 45 50	
25	aaa gca gct gag gca atg tcc act ccc aga aag gat tca gac ttc act	245
	Lys Ala Ala Glu Ala Met Ser Thr Pro Arg Lys Asp Ser Asp Phe Thr	
	55 60 65 70	
30	agg gca cag ccc aac ctg gaa cct aaa agc aag gct gtg atc gcc agt	293
	Arg Ala Gln Pro Asn Leu Glu Pro Lys Ser Lys Ala Val Ile Ala Ser	
	75 80 85	
35	gaa tgc tct gaa agc cag ctc tct aca gct tcc gca ttg aca gtc gct	341
	Glu Cys Ser Glu Ser Gln Leu Ser Thr Ala Ser Ala Leu Thr Val Ala	
	90 95 100	
40	acc gag agg ctc cag cat gtt cta gcc gct tca gac gat aag ctt acc	389
	Thr Glu Arg Leu Gln His Val Leu Ala Ala Ser Asp Asp Lys Leu Thr	
	105 110 115	
45	ctg cga cgg gaa ggc aca cag aac tca agt gac acc cta caa tcg aaa	437
	Leu Arg Arg Glu Gly Thr Gln Asn Ser Ser Asp Thr Leu Gln Ser Lys	
	120 125 130	
50	aca gct tgt gag att aac cag agt cac aag gaa tgt agg aca gag caa	485
	Thr Ala Cys Glu Ile Asn Gln Ser His Lys Glu Cys Arg Thr Glu Gln	
	135 140 145 150	
55	aca ttt gag caa cac gtg gag aag ttg ccc ttc ccc caa acc aaa ccc	533
	Thr Phe Glu Gln His Val Glu Lys Leu Pro Phe Pro Gln Thr Lys Pro	
	155 160 165	
60	att tcc ccg agt ttc aaa gtg aaa act atc agg ctt cca gct cta gat	581
	Ile Ser Pro Ser Phe Lys Val Lys Thr Ile Arg Leu Pro Ala Leu Asp	
	170 175 180	
65	cat acg ctg act gaa aca gat ctc agt tct gaa cgc cgc gta aag caa	629
	His Thr Leu Thr Glu Thr Asp Leu Ser Ser Glu Arg Arg Val Lys Gln	
	185 190 195	
70	tcc gaa att gac gtt caa acc agt act aaa gaa atg aat aag gaa att	677

Ser Glu Ile Asp Val Gln Thr Ser Thr Lys Glu Met Asn Lys Glu Ile
 200 205 210

FIGURE 11 (cont.)

5	aag aaa acc gaa gtg agc aca cag tgt gat aat aag caa tct gtg gct Lys Lys Thr Glu Val Ser Thr Gln Cys Asp Asn Lys Gln Ser Val Ala 215 220 225 230	725
10	gaa aaa tat ttt caa tta cct aaa aca gag aaa cgg gtg acg gta caa Glu Lys Tyr Phe Gln Leu Pro Lys Thr Glu Lys Arg Val Thr Val Gln 235 240 245	773
15	atg ccc aaa gac tat gca gcg aaa agt cat caa agc aaa ctc caa aca Met Pro Lys Asp Tyr Ala Ala Lys Ser His Gln Ser Lys Leu Gln Thr 250 255 260	821
20	gtt ccc aag aag cat gga gga ttg ggg gag ttt gac aga ggg aat gtc Val Pro Lys Lys His Gly Gly Leu Gly Glu Phe Asp Arg Gly Asn Val 265 270 275	869
25	ctg ggg agg gaa gga aaa aat cag gac tcc tcc atg agc agt aca aaa Leu Gly Arg Glu Gly Lys Asn Gln Asp Ser Ser Met Ser Ser Thr Lys 280 285 290	917
30	gaa agc agg gta ata gtt gaa aga aag caa gaa cat cta cag gac cag Glu Ser Arg Val Ile Val Glu Arg Lys Gln Glu His Leu Gln Asp Gln 295 300 305 310	965
35	agc gta cca agg tta gtc caa caa aag att atc ggt gaa agc ctg gac Ser Val Pro Arg Leu Val Gln Gln Lys Ile Ile Gly Glu Ser Leu Asp 315 320 325	1013
40	tca cgg gtt cag aat ttt cag cag aca caa aca caa act tct agg att Ser Arg Val Gln Asn Phe Gln Gln Thr Gln Thr Gln Thr Ser Arg Ile 330 335 340	1061
45	gag cat aaa gaa ctg tcc caa cct tac agt gag aaa aaa tgt ctt aga Glu His Lys Glu Leu Ser Gln Pro Tyr Ser Glu Lys Lys Cys Leu Arg 345 350 355	1109
50	gac aag gac aaa caa caa aaa cag gtc tcc tct aac act gac gat tca Asp Lys Asp Lys Gln Gln Lys Gln Val Ser Ser Asn Thr Asp Asp Ser 360 365 370	1157
55	aag caa gag ata aca caa aaa caa tct tca ttt tcc tct gtg aga gaa Lys Gln Glu Ile Thr Gln Lys Gln Ser Ser Phe Ser Ser Val Arg Glu 375 380 385 390	1205
60	tcc cag cag gat gga gaa aaa tgt gcc ata aaa ata ttg gaa ttc ttg Ser Gln Gln Asp Gly Glu Lys Cys Ala Ile Lys Ile Leu Glu Phe Leu 395 400 405	1253
65	aga aaa cgt gaa gaa cta cag cag att ttg tct agg gta aaa cag ttt Arg Lys Arg Glu Glu Leu Gln Gln Ile Leu Ser Arg Val Lys Gln Phe 410 415 420	1301
70	gaa gca gat tca aat aaa agt ggc ctt aaa aca ttt cag aca ctg tta	1349

Glu Ala Asp Ser Asn Lys Ser Gly Leu Lys Thr Phe Gln Thr Leu Leu
 425 430 435

FIGURE 11 (cont.)

5 aat att gct ccg gtg tgg ctg ata agt gag gag aaa aga gaa tat gga 1397
 Asn Ile Ala Pro Val Trp Leu Ile Ser Glu Glu Lys Arg Glu Tyr Gly
 440 445 450

10 gtt cgt gtt gcc atg gag aat aat tag aaaaaataaaa aaaaaaaaaa 1444
 Val Arg Val Ala Met Glu Asn Asn *
 455 460

aaaagcggcg nc 1456

15

20

25

30

35

40

45

50

55

FIGURE 12

5	gaattgtaat acgactcact atagggcgaa ttggggcccct agcgaacccc ttcgacaaca	60
	tcaaagagga cagatctaac cctagactga ggccggaggc ctggaccaat tacctgaggg	120
	atgtccacag agccttttgca ctgctgaaca gtcaccctga tccaaaccaa gtaaattgga	180
	ctccaactgc accaagcagt ggccctcccag tcacctctgc tgagctcttg gtgccggcag	240
	ag atg gct tct gca gag tca ggt gaa gac cca agt cat gtg gtt ggg	287
10	Met Ala Ser Ala Glu Ser Gly Glu Asp Pro Ser His Val Val Gly	
	1 5 10 15	
	gaa acg cct cct ttg acc ttg cca gcc aac ctc caa acc ctg cat ccg	335
	Glu Thr Pro Pro Leu Thr Leu Pro Ala Asn Leu Gln Thr Leu His Pro	
15	20 25 30	
	aac aga cca acg ttg agt cca gag aga aaa ctt gaa tgg aat aac gac	383
	Asn Arg Pro Thr Leu Ser Pro Glu Arg Lys Leu Glu Trp Asn Asn Asp	
	35 40 45	
20	att cca gaa gtg aat cgt ttg aat tct gaa cac tgg aga aaa act gag	431
	Ile Pro Glu Val Asn Arg Leu Asn Ser Glu His Trp Arg Lys Thr Glu	
	50 55 60	
25	gag cag cca gga cgg ggg gag gtg ctt ctc ccc gaa ggt gac gtc agt	479
	Glu Gln Pro Gly Arg Gly Glu Val Leu Leu Pro Glu Gly Asp Val Ser	
	65 70 75	
	ggc aac ggt atg aca gag ctg ttg ccc atc ggt cgg cac caa caa aag	527
	Gly Asn Gly Met Thr Glu Leu Leu Pro Ile Gly Arg His Gln Gln Lys	
30	80 85 90 95	
	cgt ccc cac gat gcg ggg cca gag gac cat gct ttt gaa gat caa ttg	575
	Arg Pro His Asp Ala Gly Pro Glu Asp His Ala Phe Glu Asp Gln Leu	
35	100 105 110	
	cat cct ctc gtc cac tct gac aga act ccc gtt cat cgg gtg ttc gat	623
	His Pro Leu Val His Ser Asp Arg Thr Pro Val His Arg Val Phe Asp	
	115 120 125	
40	gtg tcc cac ttg gag cag cct gtt cac tcc agc cac gtg gaa gga atg	671
	Val Ser His Leu Glu Gln Pro Val His Ser Ser His Val Glu Gly Met	
	130 135 140	
45	ttg gcc aag atg gag ggg atg gca caa agg agt ggg cac caa gtc tcg	719
	Leu Ala Lys Met Glu Gly Met Ala Gln Arg Ser Gly His Gln Val Ser	
	145 150 155	
	aag gca gcg cct cct ctc cag tca ctt ctt gct tag attacatggt	765
50	Lys Ala Ala Pro Pro Leu Gln Ser Leu Leu Ala *	
	160 165 170	
	gcctaacaat gtttctttcc atgttttgat tagtaaaacta actcgtggtg gcaatcatga	825
	ctcccaacct tctgagctcc cccgggtacg cttgcaccgt agacgctcat gtgcgcaccg	885
55	tgcggtgtgat gctcacacac agactcattg taattcaccg ttttaccgag aagggggggg	945
	gggcgaattt tctgtgttga tgctttgttt ttggtactaa aacagnatta tcttttgaat	1005
	attgtaggga catgagtata taaagtctat ccagtcaaaa tggctagaat tgngcccttg	1065

Downloaded from www.jstor.org

taagttttaa	aaacttgatg	cccacatgag	tctgtgagca	catntttccc	gcctgcctaa	1125
cggagttgga	atttgtttct	aaccactgta	attcttcaac	atcatcacct	ttggttcagt	1185

FIGURE 12 (cont.)

5	gattttgcac	tttgagtttg	gatactgtgt	ctgcttggtt	ggtagtggtta	gtatttttct	1245
	tttaaacagg	cttatcagag	ttgcacactt	tgtcctaggc	agggcaaagg	aatagacgcc	1305
	cagcaaggac	acacagtata	ggtaacatac	tgcttatcgt	acgcttttcc	cacaaagcat	1365
	tgcatgtgtt	tttacctcga	cgtgctaaag	ttgattagca	gaaaggcatg	actcacaatt	1425
	ttggtggtaa	aaaataaacc	ctgaggggagc	aagcaataac	taaaacaaga	ttgagctgct	1485
10	ctctctgtgc	ttactaaata	gatgctcgcc	ctgctaatagc	ttgccctctt	gaaagaagaa	1545
	acaggatgca	caactgcttta	tttcaatctt	ctcttttttt	tcttggtttc	accagtgagc	1605
	gtaagcattg	gaaaaaatatg	tgtagtctta	tctttctata	agacgatttt	aataaactaa	1665
	aatcacaaat	gctgtaaagt	ttgtgcgcac	cagaatggag	gctaacttca	taaacattgt	1725
	gctgtgcgaa	tattcctaaa	atgatcccca	agctgtggtt	ttctagaaga	catagttcag	1785
15	aaccgctttt	gaaaaatctg	tcctcgtgag	ctcactcagt	ttctgtcgga	cttttagaga	1845
	cagtggaaagg	attacctcat	tgagacgttt	ccgtgtcctc	ttcaactcca	cagggctctg	1905
	acggtggctt	tgtttttcct	tctagactat	tcaaacatgt	agataagtta	tatttttctt	1965
	taagtgttta	aagtaaacac	ttttcaaaaa	aaaaaaaaaa	aaaaaaaaaa	gcggccgc	2023

20
 25
 30
 35
 40
 45
 50
 55

FIGURE 13

5	tctagcgaac cccttcgggg gttttcatc	atg gag ctg tcg cgg cgg att tgt	53
		<u>Met Glu Leu Ser Arg Arg Ile Cys</u>	
		-25 -20	
10	ctc gtc cga ctg tgg ctg ttg cta ctg tca ttc tta ctg ggc ttc agc	101	
	<u>Leu Val Arg Leu Trp Leu Leu Leu Leu Ser Phe Leu Leu Gly Phe Ser</u>		
	-15 -10 -5		
15	gcg gga tct gcc ctc aac tgg cgg gaa caa gaa ggc aag gaa gta tgg	149	
	<u>Ala Gly Ser Ala Leu Asn Trp Arg Glu Gln Glu Gly Lys Glu Val Trp</u>		
	1 5 10		
20	gat tac gtg act gtt cga gag gat gca cgc atg ttc tgg tgg ctc tac	197	
	<u>Asp Tyr Val Thr Val Arg Glu Asp Ala Arg Met Phe Trp Trp Leu Tyr</u>		
	15 20 25 30		
25	tat gcc acc aac cct tgc aag aac ttc tca gag ctg cct ctg gtc atg	245	
	<u>Tyr Ala Thr Asn Pro Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met</u>		
	35 40 45		
30	tgg ctt cag ggt ggt cca ggt ggt tct agc act gga ttt gga aac ttt	293	
	<u>Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe</u>		
	50 55 60		
35	gag gaa atc ggc cct ctt gac acc cga ctc aag cca cgg aac act acc	341	
	<u>Glu Glu Ile Gly Pro Leu Asp Thr Arg Leu Lys Pro Arg Asn Thr Thr</u>		
	65 70 75		
40	tgg ctg cag tgg gcc agt ctc ctg ttc gtg gac aat cct gtg ggc acg	389	
	<u>Trp Leu Gln Trp Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr</u>		
	80 85 90		
45	ggc ttc agt tac gtg aac acg aca gat gcc tac gca aag gac ctg gac	437	
	<u>Gly Phe Ser Tyr Val Asn Thr Thr Asp Ala Tyr Ala Lys Asp Leu Asp</u>		
	95 100 105 110		
50	acg gtg gct tcc gac atg atg gtc ctc ctg aaa tcc ttc ttt gat tgt	485	
	<u>Thr Val Ala Ser Asp Met Met Val Leu Leu Lys Ser Phe Phe Asp Cys</u>		
	115 120 125		
55	cat aaa gaa ttc cag acg gtt ccg ttc tac att ttc tca gaa tcc tac	533	
	<u>His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu Ser Tyr</u>		
	130 135 140		
60	gga gga aag atg gct gct ggc atc agt tta gaa ctt cac aag gct att	581	
	<u>Gly Gly Lys Met Ala Ala Gly Ile Ser Leu Glu Leu His Lys Ala Ile</u>		
	145 150 155		
65	cag caa ggg acc atc aag tgc aac ttc tct ggg gtt gct ttg ggt gac	629	
	<u>Gln Gln Gly Thr Ile Lys Cys Asn Phe Ser Gly Val Ala Leu Gly Asp</u>		
	160 165 170		
70	tcc tgg atc tcc cct gtg gat tca gtg ctg tcc tgg gga cct tac ctg	677	

Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu
 175 180 185 190

FIGURE 13 (cont.)

5	tac agc gtg tct ctc ctt gat aat aaa ggc ttg gct gag gtg tcc gac	725
	Tyr Ser Val Ser Leu Leu Asp Asn Lys Gly Leu Ala Glu Val Ser Asp	
	195 200 205	
10	att gcg gag caa gtc ctc aat gaa aaa caa ggg ctt cta caa gga agc	773
	Ile Ala Glu Gln Val Leu Asn Glu Lys Gln Gly Leu Leu Gln Gly Ser	
	210 215 220	
15	cac tca gct gtg ggg gaa agc aga aat gat cat tga aaagaacacc	819
	His Ser Ala Val Gly Glu Ser Arg Asn Asp His *	
	225 230	
20	gacggggttaa acttctataa catcttaact aaaagcaccc ccgacacctc tatggagtcg	879
	agcctcgagt tcttccggag ccccttagtt cgtctctgtc agcgccacgt gagacaccta	939
	caaggagacg ccittaagtca gctcatgaac ggtcccatca aaaagaagct caaaattatc	999
	cctgacgacg tctcctgggg agcccagtcg tcttccgtct tcataagcat ggaagaggac	1059
	ttcatgaagc ctgtcatcga catcgtggat acgttgctgg aactcggggg caatgtgact	1119
	gtgtacaatg ggcagctgga tctcattgtg gacaccatag gtcaggagtc ctgggttcag	1179
	aagctgaagt ggccacagct gtccagattc aatcagctaa aatggaaggc cctgtacacc	1239
	gatcctaagt cttcagaaac atctgcattt gtcaagtcct atgagaacct agcgttctac	1299
25	tggatcctaa aggcgggtca catgggttcct gctgaccaag gggacatggc tctgaagatg	1359
	atgaggctgg ttactcagca ggagtagctg agctgagctg gccctggagg ccctggaggc	1419
	cctggagtag ggcccaggat gcaggtgcta atgtctatcc ccggcgctct tcttcccgac	1479
	tctaccatgg gatgtaactc caggagcccc tgccatctcc cgtaccaaaa gactgtggct	1539
	tccgtgtcta ctcagaaatc agttctactt cgtaaacagt gtttaaaacc agactcattt	1599
30	aatcagagtg aaggattgca gtccattggc ttcttagcac agaagcagct gataacacaa	1659
	gtaaacccca gcccttgaga ggtagaagca agaggatcag aggttcaagc gcatcctcgg	1719
	ctccatcaca agttcaaaaag ccgcctgcac caaatgggag tccttgtctc aaaaaaaaaa	1779
	aaaaaaaaaa aaaaagcggc cgc	1802

35

40

45

50

55

FIGURE 14

5	tctagcgaac cccttcgcga aggggttcgc taggttgcg	60
	tacctcaggg ctgtgagaac ggcactcctg atg tct gag aaa gag aaa caa gat	114
	Met Ser Glu Lys Glu Lys Gln Asp	
	1 5	
10	tgg ctg aag gat cct ccg ttc ctt cag aga cct ggg tgg aga gca tta	162
	Trp Leu Lys Asp Pro Pro Phe Leu Gln Arg Pro Gly Trp Arg Ala Leu	
	10 15 20	
	ggg aca cga aga aca gag tag cggaagaaga gttcttaagt aataagttta	213
15	Gly Thr Arg Arg Thr Glu *	
	25 30	
	cctcctgact ggctcacatc actgccttac tctgtagaaa gcaggtcatc tcatggattt	273
	ccccctccca cccccccagc tggatcattt tttgactcag ggaaaataat taaattattg	333
20	tccaactgtt agtgttgatc ggtaaagca gaaaggcaga aagttcctga taatctcaat	393
	attatctttt caaaagtatt ttcctggaat gttgtttgct ttggcattac aaagttctgt	453
	actcttaaaa atattttgac ttgctgggca tggaggtcac acctttaatc cagaggcagg	513
	catggatcca caggagttca aggccgcctg gctacaaagc gagttcaagg gcagccagg	573
	ctacacagag agaccttgct tcntnaccnn tnannaaaaa acnaaaaagc cggccgc	630
25		
30		
35		
40		
45		
50		
55		

FIGURE 15

5	tctagcgaac cccttcggta tagtccttag gtagtggcctt agtccctgga agctctgggt	60
	gcttggcatt tcaacgtgct tcttaaataa ctgttttatt agtcagtaca ag atg ctt	118
		Met Leu
		1
10	tgt ata tca gat ctg aaa tat ctt aaa att atc act tgc att gta aat	166
	Cys Ile Ser Asp Leu Lys Tyr Leu Lys Ile Ile Thr Cys Ile Val Asn	
	5 10 15	
	tac tat tcc ttt cgc aga aat aat gaa tgc ttc aag aaa aaa aaa agc	214
15	Tyr Tyr Ser Phe Arg Arg Asn Asn Glu Cys Phe Lys Lys Lys Lys Ser	
	20 25 30	
	tgt ttg tat tgg gtt taa aacgtttcca aacaccaatt attctttact	262
	Cys Leu Tyr Trp Val *	
20	35	
	taagtcatcc gatctagtta ttaaattatt attactgcct tcacactatc aaagatggta	322
	aatatctgat agaatcatat tcaaaataact tctgtttcac atttcttgag aaagtactga	382
	ctgtctgagt tctttctcaa gaaatgtgaa acagaagtat tttgaatcga aggggttcgc	442
25	tag	445
30		
35		
40		
45		
50		
55		

FIGURE 16

5	tctagcgaac	cccttcggaa	gaactgtata	tttgtgcctt	gttctgcaag	ttaaaaagct	60
	ggtccagaca	gtgtcataga	attaactttt	catctctgta	ttaatttttag	gactgcaaaa	120
	atcccaaagc	tgtatactta	gattggattc	aataaaaaag	ttaagtttac	tnaanaaaaa	180
	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaanaaaaa	aaaaaaaaag	240
	aaaaaaaaaa	ncggncnnaa	aaaaggnggc	cgc			273

10

15

20

25

30

35

40

45

50

55

FIGURE 17

5	tctagcgaac	cccttcgggg	gaacccaagc	ggcttcgccc	aggcattcgc	gcgggcgccc	60
	gcggtctggg	tcccacctcc	tctgctttcg	cacccttgaa	gttttgagc	accaggaaaa	120
	gagggcaagg	aaggagagg	gaagcgaaag	catatcctaa	aacatttact	taaaggagga	180
	aagaaaagg	gtcgcagaa	atg gct ggg	gca att ata	gaa aac atg	agc acc	232
			Met Ala Gly	Ala Ile Ile	Glu Asn Met	Ser Thr	
10			1	5		10	
	aag aag ctc	tgc att gtt	gga ggg att	ctt ctg gtt	ttc caa atc	gtt	280
	Lys Lys Leu	Cys Ile Val	Gly Gly Ile	Leu Leu Val	Phe Gln Ile	Val	
		15		20		25	
15	gcc ttt ctg	gtg gga ggc	ttg atc gct	cca gca ccc	aca acg gca	gtg	328
	Ala Phe Leu	Val Gly Gly	Leu Ile Ala	Pro Ala Pro	Thr Thr Ala	Val	
		30		35		40	
20	tcc tac gtg	gca gca aaa	tgt gtg gat	gtc cgg aag	aac cac cat	aaa	376
	Ser Tyr Val	Ala Ala Lys	Cys Val Asp	Val Arg Lys	Asn His His	Lys	
		45		50		55	
25	aca aga tgg	ctg atg ccc	tgg gga cca	aac aag tgt	aac aag atc	aat	424
	Thr Arg Trp	Leu Met Pro	Trp Gly Pro	Asn Lys Cys	Asn Lys Ile	Asn	
		60		65		70	
30	gac ttc gaa	gaa gca att	cca agg gaa	att gaa gcg	aat gac att	gtg	472
	Asp Phe Glu	Glu Ala Ile	Pro Arg Glu	Ile Glu Ala	Asn Asp Ile	Val	
		80		85		90	
35	ttt tct gta	cac att ccc	ctc cct tct	atg gag atg	agc cca tgg	ttc	520
	Phe Ser Val	His Ile Pro	Leu Pro Ser	Met Glu Met	Ser Pro Trp	Phe	
		95		100		105	
40	cag ttt atg	ctg ttt atc	ctg cag ata	gac att gct	ttc aag cta	aac	568
	Gln Phe Met	Leu Phe Ile	Leu Gln Ile	Asp Ile Ala	Phe Lys Leu	Asn	
		110		115		120	
45	aac caa atc	aga gaa aat	gca gaa gtt	tcc atg gat	gtt tcc ctg	ggc	616
	Asn Gln Ile	Arg Glu Asn	Ala Glu Val	Ser Met Asp	Val Ser Leu	Gly	
		125		130		135	
50	tac cgt gat	gat atg ttt	tct gag tgg	act gaa atg	gcg cac gaa	aga	664
	Tyr Arg Asp	Asp Met Phe	Ser Glu Trp	Thr Glu Met	Ala His Glu	Arg	
		140		145		150	
55	gta cca cgt	aaa ctc aga	tgc act ttc	aca tcc ccc	aag acc cca	gag	712
	Val Pro Arg	Lys Leu Arg	Cys Thr Phe	Thr Ser Pro	Lys Thr Pro	Glu	
		160		165		170	
60	cat gaa ggt	cgt cat tat	gaa tgt gat	gtc ctt cct	ttc atg gaa	att	760
	His Glu Gly	Arg His Tyr	Glu Cys Asp	Val Leu Pro	Phe Met Glu	Ile	
		175		180		185	
65	ggg tca gtg	gct cat aag	tat tac ctt	cta aat atc	cgg cta cct	gta	808
	Gly Ser Val	Ala His Lys	Tyr Tyr Leu	Leu Asn Ile	Arg Leu Pro	Val	

190

195

200

FIGURE 17 (cont.)

5	aat gag aag aag aaa atc aat gtt gga att ggg gaa ata aag gac att	856
	Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile	
	205 210 215	
10	cgg ttg gtg gga atc cac caa aat gga ggt ttc act aag gta tgg ttt	904
	Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe	
	220 225 230 235	
15	gct atg aag acc ttc ctc aca ccc agc atc ttc atc att atg gtg tgg	952
	Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp	
	240 245 250	
20	tat tgg aga agg atc acc atg atg tcc cga cct cca gtg ctt ctg gaa	1000
	Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu	
	255 260 265	
25	aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc aat atc cct	1048
	Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro	
	270 275 280	
30	gtg gaa tgg ttt tcc att gga ttt gat tgg acc tgg atg ctg tta ttt	1096
	Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe	
	285 290 295	
35	ggt gac ata cga cag ggc atc ttc tat gca atg ctt ctt tcc ttc tgg	1144
	Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp	
	300 305 310 315	
40	atc atc ttc tgt ggc gag cac atg atg gat caa cat gag cgg aat cac	1192
	Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His	
	320 325 330	
45	att gca ggg tat tgg aag caa gtt gga cca att gct gtt ggc tct ttc	1240
	Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe	
	335 340 345	
50	tgc ctc ttc ata ttt gac atg tgt gag aga gga gtg caa ctc aca aat	1288
	Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn	
	350 355 360	
55	cct ttc tac agt atc tgg act aca gat gtt gga aca gaa ctg gct atg	1336
	Pro Phe Tyr Ser Ile Trp Thr Thr Asp Val Gly Thr Glu Leu Ala Met	
	365 370 375	
60	gct ttc atc att gtg gca ggt atc tgc ctc tgc ctc tac ttc ctg ttt	1384
	Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe	
	380 385 390 395	
65	ctg tgt ttc atg gta ttt caa gta ttc aga aac atc agt ggg aaa cag	1432
	Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln	
	400 405 410	
70	tct agc ctc cca gcc atg agc aaa gtc cgg agg ctg cac tat gag ggt	1480

Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly
 415 420 425

FIGURE 17 (cont.)

5	ctg att ttc agg ttc aag ttc ctc atg ctg atc acc ttg gct tgt gct	1528
	Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala	
	430 435 440	
10	gcc atg act gtt atc ttc ttc att gtt agt cag gtg aca gaa ggc cat	1576
	Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His	
	445 450 455	
15	tgg aaa tgg ggt ggg gtc aca gtt caa gtg agc agt gct ttc ttc act	1624
	Trp Lys Trp Gly Gly Val Thr Val Gln Val Ser Ser Ala Phe Phe Thr	
	460 465 470 475	
20	gga atc tat ggg atg tgg aac ctg tat gtc ttt gct ttg atg ttc ttg	1672
	Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu	
	480 485 490	
25	tat gca cca tcc cat aag aac tat ggg gaa gac cag tct aat ggt gac	1720
	Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Asp	
	495 500 505	
30	ctg ggt gtc cac agc ggg gaa gaa ctg cag ctc act acc aca atc acc	1768
	Leu Gly Val His Ser Gly Glu Glu Leu Gln Leu Thr Thr Thr Ile Thr	
	510 515 520	
35	cat gta gat gga ccg act gag atc tac aag ttg acc cgt aaa gaa gca	1816
	His Val Asp Gly Pro Thr Glu Ile Tyr Lys Leu Thr Arg Lys Glu Ala	
	525 530 535	
40	cag gag tag taggctatgg cattcatcct cagggcaggt gatgaagcca	1865
	Gln Glu *	
	540	
	agttgctggt gcatgctgac cctcatgaat atgctttcgt atctttatgt cccaggatca	1925
	ttttatcct gtcacgttta caagaacatt tctgacatgc atacgtttac ttttaccatg	1985
	tattagttac ttttatatatt ctgtgataaa acaccatgag aaatacaatt tacagaagca	2045
	aaaaaaaaa aaaaaaaaaa aaaagcggcc gc	2077

45

50

55

FIGURE 18

5	tctaacgaac cccttcggag cgatgga atg aga aag gcc cag aat gtg tta agt	54
	Met Arg Lys Ala Gln Asn Val Leu Ser	
	1 5	
10	ctg tgc agg gga agt gtc ctg agg gga ggg tct ttg gga ggg tcg aag	102
	Leu Cys Arg Gly Ser Val Leu Arg Gly Gly Ser Leu Gly Gly Ser Lys	
	10 15 20 25	
	gcc agg atg gca aag tga aggtagctga ggttgacgtc ttgggtgccc	150
15	Ala Arg Met Ala Lys *	
	30	
	actgctgtgc atctgtcttg ttatctaccc ctactttggg ctgacaactg cagggttggg	210
	tgtaggctgt ctcaactgcat gccgggaagc tggagaagct ccacgggaac attgagggcc	270
20	atggctttga gacactgcag agcatccttg gtctctgtaa ccacgtcacc taaccctgac	330
	aattccagac ccttcttcca ttgtccttgt gaaccatttg ggcttatctt tccctcttag	390
	tcgcaagggt caaaccaagg gtcagtcaag tagatgactg tcaccttggg cctccccaga	450
	ctctgctgcc ggggttggga gaccaaagta gaaactgcca ctacaaggcc ccaggatgag	510
	gtctctgttc tgttgacctg ctccccagat acaggcctca gacctatagg acgtggcccg	570
25	tgctcaggga cacccaatcc ccggcctcac tccatcgagt actgacttct ttctctagt	630
	ccttgggggt ctccatcctt cagttatggt atgaagaatc tatgcaaact gtataagctt	690
	ctgctcacca ataaacgctt tatttaaagc ttannnnnnn nnnannnnnn nnnnnaagcg	750
	gncgc	755
30		
35		
40		
45		
50		
55		

FIGURE 19

5	tctagcgaac cccttcgcag aaacccaaag ttacagacca gaccctaccc aacatccagt	60
	cagcaatcca gctggagaaa cgcttgag atg aca agg gac ttt cag aag caa	112
	Met Thr Arg Asp Phe Gln Lys Gln	
	1 5	
10	gcc ttg ata aga cag gaa aag cag aat tct aat aaa gat atg agg aaa	160
	Ala Leu Ile Arg Gln Glu Lys Gln Asn Ser Asn Lys Asp Met Arg Lys	
	10 15 20	
	aat gac atg ggc ctt caa cct ctg cct gta ggg aag gac gca cac agt	208
15	Asn Asp Met Gly Leu Gln Pro Leu Pro Val Gly Lys Asp Ala His Ser	
	25 30 35 40	
	gca cca gga gtg aca gtc tct ggg aaa aac cac aaa aga act cag gca	256
	Ala Pro Gly Val Thr Val Ser Gly Lys Asn His Lys Arg Thr Gln Ala	
20	45 50 55	
	cct gac aag aaa cag aga att gat gtt tgt cta gaa agc cag gac ttt	304
	Pro Asp Lys Lys Gln Arg Ile Asp Val Cys Leu Glu Ser Gln Asp Phe	
	60 65 70	
25	cta atg aag aca aat act tcc aag gag tta aaa atg gca atg gag agg	352
	Leu Met Lys Thr Asn Thr Ser Lys Glu Leu Lys Met Ala Met Glu Arg	
	75 80 85	
30	tcc ttt aat cca gtc aac ctt tcc ctg act gtg gtg taa aagaaaatga	401
	Ser Phe Asn Pro Val Asn Leu Ser Leu Thr Val Val *	
	90 95 100	
35	ggacgccctt ctctccatct tcccctcctt cttctccttc caattgcgtc atctgaaatt	461
	gaatttcctc tctcctcca ccacctataa tgctgtgcct gaaaaaaatg agtttcctcc	521
	ctcatcaccc acagagaaagt caagggctga acttgagagc ctccaaccc tgcctcttcc	581
	tccaccacca ggagatgaga aatctgatca ggaatgtcta ccaacatccc tacctcctcc	641
	ccctcccaca gctccatccc aaccagcaca tcttctttcc tctctgttc tagaacatca	701
	cagtgaagca tttttacaac agtattcccg aaaagaaacc ttggactctc atcggttca	761
40	ctcacaggct aaaatcctaa caggaaaaatc accacccccca aactccccca aacccaaact	821
	tcccgagaga atcaaagcta agatgagcca ggattcacca agcgggtgaat tggaaagatc	881
	tctgtcagat gtggaaatta aaactaccct ctcaaaggat cagaaaagtt cgctggtggc	941
	agaaagccgt gagcacacag aggccaagca agaagtattc cgaaaaagcc ttggaagaaa	1001
	acagctgtcc attagctctg caaactccct ctctcagaca gttccagaaa tcccagcacc	1061
45	caaggaaaaa cagacagcac cccttggttaa atctcactca ttcccatcag gttcagaaca	1121
	acaaagtccct aagccttaca tgagaaaaatt taagacaccc ttaatgattg cggaagaaaa	1181
	atacagacaa caaaggggaa agcttgagaa acagagacgg gagagtctt gccatagcat	1241
	catcaaaaaca gaaacccagc accgcagctt atcaaanntt aaaaaaaaaa aaannnagc	1301
	ggnccgcccc	1310
50		
55		

FIGURE 20

5 tctagcgaac cccttcgctt tttttttttt tttttttttt ttttccccc tttcctatatt 60
 attaatgggg ggaagtatgt ttatgtggga tttatccact tcttttagat tctcctacct 120
 gttgatctgt aattattcct agtagtctct tagagttctt agaagcatgc tgttaccgct 180
 aatatttcct tttggtttgg atcttactta aacatattgt ttccttactc tctttttcat 240
 ccagcttgt ctaactgaaa ggccagaccc aacttgatct atccctttaa aacttc atg 299
 Met
 10 .1

tct tgg cct gtt gat ttc tct gct cca ggt gtc acc gaa ggg gtt cgc 347
 Ser Trp Pro Val Asp Phe Ser Ala Pro Gly Val Thr Glu Gly Val Arg
 15 5 10 15

cta gcg aac ccc ttc gta aca gcc aag gtt ttt gag aca gag gtt tca 395
 Leu Ala Asn Pro Phe Val Thr Ala Lys Val Phe Glu Thr Glu Val Ser
 20 20 25 30

aca gca ttc ctg gag gag aca caa agg aca gat gag tca cat gaa gga 443
 Thr Ala Phe Leu Glu Glu Thr Gln Arg Thr Asp Glu Ser His Glu Gly
 35 40 45

tgg gag gag gga agg tgg ctg ttg ata ggt att ttg aga cac tct att 491
 Trp Glu Glu Gly Arg Trp Leu Leu Ile Gly Ile Leu Arg His Ser Ile
 50 55 60 65

tga gtcctacaca acactccccc ctccccccaa accatttttta tgtctattga 544
 30 *

cctttcctct agtcatacag ggaaattcac agttacctac aaagaaccac taattgtaac 604
 aagtcaagag gaaacttatt tttgataatg actcattgaa gatgttttga aaatttaaaa 664
 35 ataagctctg ttagcagaag tctgtnnngaa aagcangaag gaantgtttg tttattanat 724
 aaataaaaagg cggcgaggac aacaaaaaaa aaaaaaaaaa aagcggccgc 774

40

45

50

55

FIGURE 21

5	tctagcgaac cccttcgcga aggggttcgc cgaaggggtt cgcttcagga gttaatgtag	60
	acttgactta agcatcctga tttaaccaag a atg gtg gca cac aac ttt aac	112
	Met Val Ala His Asn Phe Asn	
	1 5	
10	ccc cat gct ggg gaa gca gag gca cac tta atc tgt gtg agt ccc agg	160
	Pro His Ala Gly Glu Ala Glu Ala His Leu Ile Cys Val Ser Pro Arg	
	10 15 20	
	cca tcc agg gat acc gta gta gtg aga ccc tgt gtc aca aaa caa aga	208
15	Pro Ser Arg Asp Thr Val Val Val Arg Pro Cys Leu Thr Lys Gln Arg	
	25 30 35	
	atg gga att tag ggctgggtggg gctcagcatg caactgtgcc tgttacctag	260
	Met Gly Ile *	
20	40	
	tctggcctga gttcaattcc caagactcaa tgtatgagga gagaaacgat ttctgaactc	320
	attcattgat ctccaaatgt gtggtatagg tgcccttccc ttaaataaaa caaacaacaa	380
	aaaaacaaca aaaacaacaa accccaata aatgtatatt taattttaaa agactgtact	440
25	tgggcatggt acttcacatc tacagttacg acattctaga ggctcaggcc tgggaattgc	500
	tatgaatttg aggccagtct gggttagagt gacttctcat ctaggcagga ctacgtaata	560
	agtctttgcc caaaaataaaa cagcaaccca aataagagca acaagaattc tccctccaaa	620
	tagtaacctg ggctgggaga gacagcttag caactgagtg cttgccgagc catcgaggac	680
	tggagtctgg attccagcac ccgtgtgaca gacaagctgg gcgttcactc atgctgatga	740
30	acccaaggc tgaggagaca ctgactcttc tctggccctg ttcatgctgt ccacaggtgc	800
	ccaagtagca gttaagtaga ctgtcagaca acatggctgg ctttttaagc aagaacagta	860
	actgaagaaa tacacttttg aagtactggt aattttgctt aaaacttggt agggagctgg	920
	aggatggctc agtggttaag agcactgact gctcttcag aggtcctgag ttcaattccc	980
	agcaaccaca tgggtggctca caaccatctg taatgagctc tgatgccctc tttttggtgt	1040
35	gtctgaagac agcgacagtg tactcatata aaataaaaata aatctttttt ttttttaaaa	1100
	gaaatttgtc agagatatgg caggaagggt atatttttac ctattttacct ggtgggctaa	1160
	tcctgggtatt tttttcaaaa ttaagatact atataggagc cgcaagggg tcgctaggcc	1220
	agtgtgatgg atatctgcag aattcgggta gccgaattc	1259
40		
45		
50		
55		

FIGURE 22

5	tctagcgaac	cccttcgtct	cctcttaaac	atcttaagac	aagctgttat	catctacact	60
	gctcttagta	ctgttctttt	ctaagattct	tctaatatga	cacattaaga	ctttcttaaa	120
	atgtacaact	gctacgctga	tctaaacatt	caaagtgcac	acatttcgct	atgaagccac	180
	gtgaccagag	tcctggggac	taatttctgt	cttagtcaga	ttcctattgc	tatatgaaga	240
	aatacc atg	ata gtg tca	act ttt ata	aag aaa aag	tat tcc ttt	ggg	288
10	Met	Ile Val	Ser Thr	Phe Ile	Lys Lys	Lys Tyr Ser	Phe Gly
	1		5		10		
	aat agt tta	aag gat cag	agg gtt agt	gca tta tca	tca tca cag	cag gaa	336
	Asn Ser Leu	Lys Asp Gln	Arg Val Ser	Ala Leu Ser	Ser Ser Gln	Gln Glu	
15	15		20		25		30
	gcg tgg cag	tgg gag ccc	aga ttt cta	tat cca gat	ttt cat gaa	gca	384
	Ala Trp Gln	Trp Glu Pro	Arg Phe Leu	Tyr Pro Asp	Phe His Glu	Ala	
		35		40		45	
20	tga cgagagctcc	tgggcctggc	gcgagcttct	gaaacctgaa	agtgacatat		437
	*						
25	ttcttccaat	aaggccacaa	ctactgctat	aaggccacat	ctcctaactg	tgtcactatc	497
	tatgagcctg	tacagtctat	ttctttttaca	ccactgcatc	atctaagagc	tgatacccgct	557
	taagttagtc	atgaaaatat	tcaacttcta	gggttctgtt	ttcttctcta	taaaatattg	617
	aaaatgataa	ttaatgtata	ctttacagaa	ctgtatttga	agtacaactt	gatggacata	677
	aatcaccaca	gttgggtcaa	aattgtatat	atatatatat	atatatatat	atatatatat	737
30	atatatcaaa	aaaaaaaaaa	aaaaaaaaaa	aagcggccgc			777
35							
40							
45							
50							
55							

FIGURE 23

5	tctagcgaac	cccttcgtac	atttcaccct	agaaataaat	agaccttcta	gctctgacag	60
	aaagtagtgc	ttgcctagga	ggagctgggc	tggccagttc	ctccttcttg	cacacttagc	120
	ctgtttgctg	aaggcttggt	tcaatggaaa	actgaaatgg	accactaat	gtctcgattc	180
	ttctctcctt	cactaagtct	gtgaagtcac	cagcgttttg	tcttttggtg	gtgaataccg	240
	aggagaattt	cctcaccag	tgccttcagg	agccatgatg	gctgcctcag	aataagcaca	300
10	gatacacttg	agcaactggg	gcagaaaacc	cgacttctaa	attattaagg	aacaggataa	360
	ttgcttggtt	caataattag	aataatgtaa	ttaggataat	tgcttttaaa	aaatcttccc	420
	acctttcccc	ccccaaatat	taataattcc	aactaaatcc	tctggggccc	ttccagtttc	480
	cacaacggaa	agagcctaac	gtatttctaaa	gactgggcat	attttttttt	tccagattag	540
	tgagtgttca	tgagctatta	agaggccaag	tgttttttca	agatgggtgc	atttcattct	600
15	aacatatcta	acatgcaaag	gacttaaaaa	aataatttgc	aaaataatct	gtttcaagtc	660
	tatgaggaag	ctgaagagcc	tactccggag	gaaactccag	aagagcctcc	tagcatagag	720
	gaagaagaga	tagtggagga	agaggaggag	gaggaggtgc	ccccgcccag	aggtacagcc	780
	gctttgatga	gttcagcatt	ccaaagcctt	ggtgctgctg	gaccctactc	attagccata	840
	tactttcctg	gaagcacagc	cacgaggcct	ggagggtgca	cactcgtaac	gactggagct	900
20	ttgtgggcct	ttcctttccc	ctaacgtttc	ctccttcccc	gcaatctgac	cataaatgag	960
	gagatttttt	ttttctctta	ctacactttt	tgcaatccta	gtttgcaatc	ctcagtgtgg	1020
	ctggctttca	gttcaaagtc	tggagaacca	tgtatctgtg	tggtgagagc	attcattttc	1080
	aagactaatt	cttaaaccgc	ttatccccgg	agacagaaac	cgtggcagag	ttgctatcct	1140
	ctgagctggg	gtgggtcatga	tgatcagtta	ggttactaac	atcttcctaa	atgaatcggg	1200
25	gttttggtgt	gctctgtttt	catttggtatg	acagggtgtt	gttctgttta	atgctgtgtg	1260
	gtttttccaa	catgtccgta	aaaatatcct	ttaagcacca	gangtagtga	agaaagctgt	1320
	gcaaacagca	cccgtcctg	tccccaaaga	awccgaggcg	cccccccaa	ggtatatac	1378
30							
35							
40							
45							
50							
55							

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 24

5	tctagcgaac cccttcgcga accccttcgc tgcattcctca taaagctacc tcaagacaga	60
	gcgtaactgc ctcattctag gagtggactc ggggaagaca gcagacacac catcagggag	120
	cccctgggta tctccagaac atg gca agc cgt gga tac ctg cat cac ctg ctg	173
	Met Ala Ser Arg Gly Tyr Leu His His Leu Leu	
	1 5 10	
10	act gca gag gga gcc tgg gag gag ttt gta tca aag gcc aag ttg ccc	221
	Thr Ala Glu Gly Ala Trp Glu Glu Phe Val Ser Lys Ala Lys Leu Pro	
	15 20 25	
15	agg gat agg gca gtg gcc ctc cac aaa gca ctg agg gat ctg aca gca	269
	Arg Asp Arg Ala Val Ala Leu His Lys Ala Leu Arg Asp Leu Thr Ala	
	30 35 40	
20	ctc ttg gcc ata gca gaa aga ggc aga tct cgg aaa ggc ttg aaa ggc	317
	Leu Leu Ala Ile Ala Glu Arg Gly Arg Ser Arg Lys Gly Trp Lys Gly	
	45 50 55	
25	aag gag aag ttt gtg aaa gca ttt cct tgc ttg aaa gca gac ttg gag	365
	Lys Glu Lys Phe Val Lys Ala Phe Pro Cys Leu Lys Ala Asp Leu Glu	
	60 65 70 75	
30	gag cac atc agc cag ctc tat gcc cta gcc gac cat gct gag gaa ctg	413
	Glu His Ile Ser Gln Leu Tyr Ala Leu Ala Asp His Ala Glu Glu Leu	
	80 85 90	
35	cac agg ggc tgc acc gtc tcc aac atg gtg gct gac tcc ttc agt gtt	461
	His Arg Gly Cys Thr Val Ser Asn Met Val Ala Asp Ser Phe Ser Val	
	95 100 105	
40	gcc tcc gac atc ctg aac atc ttt ggt ctc ttt ctg gca cct gag tca	509
	Ala Ser Asp Ile Leu Asn Ile Phe Gly Leu Phe Leu Ala Pro Glu Ser	
	110 115 120	
45	gca gag gga agt ctg gtg ctc tcg gca gca ggc ttg ggg ctg ggg gta	557
	Ala Glu Gly Ser Leu Val Leu Ser Ala Ala Gly Leu Gly Leu Gly Val	
	125 130 135	
50	gca gct act gtg act aat gtt gct act tca atc atg aag gaa aca agc	605
	Ala Ala Thr Val Thr Asn Val Ala Thr Ser Ile Met Lys Glu Thr Ser	
	140 145 150 155	
55	agg gtt ttg gat gga gtc gaa gct ggt cac cat ggt tca acc gcc atg	653
	Arg Val Leu Asp Gly Val Glu Ala Gly His His Gly Ser Thr Ala Met	
	160 165 170	
60	gat ata ctg gag gaa gct ggc aca agt gtg gct agg att gcc agc gag	701
	Asp Ile Leu Glu Glu Ala Gly Thr Ser Val Ala Arg Ile Ala Ser Glu	
	175 180 185	
65	atc cct cag gct acc aga gat atc acc aga gac ctg gaa gcc ctt gag	749
	Ile Pro Gln Ala Thr Arg Asp Ile Thr Arg Asp Leu Glu Ala Leu Glu	
	190 195 200	

cag cac atg aat gcc ctc agt ctg gtc aga gcc aac cct cgc cta gaa 797
FIGURE 24 (cont.)

5	Gln His Met Asn Ala Leu Ser Leu Val Arg Ala Asn Pro Arg Leu Glu 205 210 215	
10	gaa gat gcc agg gcc ctc atc aat gca ggt agc atc cct gcc caa cgg Glu Asp Ala Arg Ala Leu Ile Asn Ala Gly Ser Ile Pro Ala Gln Arg 220 225 230 235	845
15	gct aaa cag gtg cgg gcc agt ctg aaa gga acc cct ctg gca atg agc Ala Lys Gln Val Arg Ala Ser Leu Lys Gly Thr Pro Leu Ala Met Ser 240 245 250	893
20	aag gaa gac cgg atc cgc agt gcc acc acc act ggg gtc acc ctc ttg Lys Glu Asp Arg Ile Arg Ser Ala Thr Thr Thr Gly Val Thr Leu Leu 255 260 265	941
25	cgt gat gtg ggg agc ctt gtg aac gag tcg aag cag ttg tac gaa ggg Arg Asp Val Gly Ser Leu Val Asn Glu Ser Lys Gln Leu Tyr Glu Gly 270 275 280	989
30	tct gct tcc gaa tcg gca gca gca cta agg aag ctg gct cag gag ctg Ser Ala Ser Glu Ser Ala Ala Ala Leu Arg Lys Leu Ala Gln Glu Leu 285 290 295	1037
35	gag gag aag cta ggg gag ctc atg aaa ttc tac gag aca atc tga Glu Glu Lys Leu Gly Glu Leu Met Lys Phe Tyr Glu Thr Ile *	1082
40	tcagggtttca gccagtcacc ccatcccca gacatgcaga catcanggga gaggatctgg acagaggttag ggaccatgga ggtgctgtta gaaggagagc aagactacag tcagggtccga gggacatagt gtggaggcct gtttgatgaa cacarcaggt taraggatgg agcagtggat caaagtgaga tccactggag cctgagacsa gggaccagag gatgtgctgc aagagggact gggaaaattg aaatctanac taaacatgga aaaaaggcag ttctgaaaga ctagaaaacc ctccccatct gagccattgg aaaccccaca aaacacaaac cagagagaaa agtgtgtgct ctctaaacaa gtcgtggccc ccagttcccc agcccactcc caccctcagg ggtggcatca aataaattgt ttccatttca aaaaaaaaaa naaanaaaaaa aaaagcggcc gc	1142 1202 1262 1322 1382 1442 1502 1554
45		
50		
55		

FIGURE 25

5	tctagcgaac	cccttcggct	ttttctgatt	taaagtgaag	aaatggccat	atttgcttga	60
	taatcttcag	ttgtgtctct	ggaactcaac	aaagaacgca	ttttatgaaa	tatacagctg	120
	tcttcggtaa	agccaacttt	cttacacata	tttcgggaag	taatttaacta	caatttggac	180
	ttatagttac	aaggttgcct	tcgaaacact	gctctaaatg	tgtctcgtgt	tggggtgcta	240
	ctttgcttat	gtgtaaattt	cacagtaatg	caatagagaa	aggggtgttg	tgggtgtggc	300
10	ttgtgggggg	gattgttttg	ttgttgttgt	ttgagataaa	gcttcattct	gtagccagga	360
	aagcctggaa	tttactgtgt	catcccaggt	agcttcaaac	tgggtgcctat	cctgcctcag	420
	cctccaacgt	gttgcaattg	caggagtaac	ctaccacatc	ctgcagctac	agtgatctag	480
	aacctccccg	tcgaagcccc	accaccatag	aaaccaattt	gcattaagtt	ttagaattcc	540
	caacccaact	aaagtttaat	aaaaaaaagaa	aaacaaaaca	agatttaaat	cattctttcc	600
15	ctcattcttt	ttnnagatnc	agggctcncc	tagttttnaa	caaaacagtn	ngcagnng	660
	ggnnccccng	gnngggnttt	tttncnttgn	gccnctnngc	anccccccn	cccaggcnng	720
	atngggnggg	gtataaaaagt	nttanccngc	anatgnnctn	ggngcanacc	caagtntatc	780
	aggncctnan	ttncncccca	ganaactaga	nancntnngc	atagtanang	ccccntgtgn	840
	agatttnaaa	nccnccgtgn	cacaganana	gaancttana	tagaaaantc	aaaatatttn	900
20	ggngcccaan	gttnccacc	ctgtagagng	ggnccccana	ancngccncc	aganagcnng	960
	atatntgagt	tntgacctnt	attctttact	acnacgcntt	gagagaatat	tntgntgggg	1020
	ccctanccac	atgttttgnc	ccaagantgt	aaanccactt	naannctgng	ggatatctcn	1080
	ctgcanacag	aagtgcccn	cgggatttta	aaaaaaaaaa	taaaaaaaaa	aaaggngccn	1140
	cc						1142

5
10
15
20
25
30
35
40
45
50
55

FIGURE 26

5	tctagcgaac	cccttcgtgg	agactgtgga	agttatgtat	gaataggaga	gtgtgtgttg	60
	tgtaacacag	acagaaggac	attggatcat	gttgaacccg	caccccccaac	tatgagtgat	120
	ggtatggaaa	gaatgcgaac	atttaaaactg	cgccaatgcg	gcggccatct	tgggtggagaa	180
	gttcctagcc	gagctttgat	gtgatttttt	tgatggtaca	atgcagcgag	catggccacg	240
	ggagctttga	atccagccga	cagctccgag	atttgccctt	ccagtgtctt	tgcctaccgt	300
10	agagaggact	gctgagatgg	gattccttgt	gacaagccta	cttaccttta	actgccagca	360
	tttgtaaggt	gcaatcttgt	gtattggttt	tttattttga	cagttttgaa	aacatgtttg	420
	ntgntcttgg	tgtttttcca	gtaaaaagtaa	tcacaaagga	aaaaaaaaatt	aaaaaaaaaaa	480
	aaaaaaaaaaa	aaaagcggcc	gc				502

15

20

25

30

35

40

45

50

55

FIGURE 27

5	tctagcgaac	cccttgcgct	tcatatggtt	ttacactgta	tgcattctcac	cgcgggccgg	60
	aaccttttctt	ctcatcccaa	tctgttttga	ggggacgggg	ggcaggggacg	gacaacccaa	120
	gacaagggat	atttgtgtctg	tgggtattgc	atcttatgga	gggctgtagc	taactgggac	180
	tcttgggtga	ccccaacagg	cccttgatcc	tctgtctctc	cccgttgat	ctttcttacc	240
	ttatgcttcc	ccaagtgcag	ctgagggact	acacagtggc	tcccgcccca	ctccaaacac	300
10	aggaaatcaa	tctcaggggag	aggagataag	aagtgaggag	aagccaagat	tcaaccaata	360
	gatggtaatt	gctcctggga	ccgccccccc	aagcatcatt	tccataggaa	ggactgagtt	420
	tggctcctga	agcccagtg	agtaccttcc	tctgcctgaa	ttctgttg	atccctggcc	480
	aagtcctctt	tccagaaacc	ccacctttaa	aaccagctga	gaaggacctt	cttctctatg	540
	tttaataggt	aactttccat	agcttagctt	ccctgcagtc	tcccgagtgc	ccagttaaaa	600
15	ttctgccata	ggtcaaaagt	ggggttgaga	ggtgaagtca	gaggccatgc	atggagctca	660
	gaacgtttct	aaacctcctg	tgattcattg	agtagcccct	agactctaga	aggctcagat	720
	gcaaaaaagg	ktgactttat	aatttcttag	ggtcttctca	tgggatcgkt	ttcagagtg	780
	gcattcacta	aatgatagca	agttttattaa	ttgtttccca	gygcctgac	tctttatttn	840
	cccagggtct	ccaaccagag	cccttggttg	aaagtctccc	acccaccccc	caccttgaga	900
20	cttgggtgnt	ttctgagatt	cccagggat	ggcaaaattg	gcattcttac	agggagccct	960
	gacttctagc	acgttaccta	gattttttac	cctgctctct	ctgcctat	tactatggga	1020
	tcactgntct	ctttggactt	aaggaaccac	cttgaagtga	agtgaagtga	ccacgtgttg	1080
	gtggcggaaga	atataagcat	tggtccttaa	aagagaactt	ctatgaagtc	aggctgcaag	1140
	ctttaacatg	gcacaagttg	caccttactg	gctgctaagt	ctgtagtca	accaaaggtc	1200
25	aactctntaa	ttaaagaaaa	gcaagggaga	aganaggtgg	aangngcttn	cataaaacttt	1260
	attcaaaatg	tctaccagga	atgggtggtga	caccaataat	cccacatgtt	ggatgtngag	1320
	gcaggaagaa	tgatggtgta	gggcacctc	actacataat	gagttgaggg	tngactaggt	1380
	taactntgct	tnaaaaaaaa	aaaaaaaaaa	aaaaaaaaagg	gnggcc		1426

12	18	24	30	36	42	48	54	60	66	72	78	84	90	96	102	108	114	120	126	132	138	144	150	156	162	168	174	180	186	192	198	204	210	216	222	228	234	240	246	252	258	264	270	276	282	288	294	300	306	312	318	324	330	336	342	348	354	360	366	372	378	384	390	396	402	408	414	420	426	432	438	444	450	456	462	468	474	480	486	492	498	504	510	516	522	528	534	540	546	552	558	564	570	576	582	588	594	600	606	612	618	624	630	636	642	648	654	660	666	672	678	684	690	696	702	708	714	720	726	732	738	744	750	756	762	768	774	780	786	792	798	804	810	816	822	828	834	840	846	852	858	864	870	876	882	888	894	900	906	912	918	924	930	936	942	948	954	960	966	972	978	984	990	996	1000
12	18	24	30	36	42	48	54	60	66	72	78	84	90	96	102	108	114	120	126	132	138	144	150	156	162	168	174	180	186	192	198	204	210	216	222	228	234	240	246	252	258	264	270	276	282	288	294	300	306	312	318	324	330	336	342	348	354	360	366	372	378	384	390	396	402	408	414	420	426	432	438	444	450	456	462	468	474	480	486	492	498	504	510	516	522	528	534	540	546	552	558	564	570	576	582	588	594	600	606	612	618	624	630	636	642	648	654	660	666	672	678	684	690	696	702	708	714	720	726	732	738	744	750	756	762	768	774	780	786	792	798	804	810	816	822	828	834	840	846	852	858	864	870	876	882	888	894	900	906	912	918	924	930	936	942	948	954	960	966	972	978	984	990	996	1000

30

35

40

45

50

55

FIGURE 28

5	tctagcgaac cccttcgcaa gaactcagac tgctcctgcc tgacttccta ggtgtcatag	60
	ctctcttctg ccgccagt atg aca tca tca agg aca acg agc cca ata aca	111
	Met Thr Ser Ser Arg Thr Thr Ser Pro Ile Thr	
	1 5 10	
10	aca agg aaa aaa cca aga gtg cat cag aga cca gca ccc cag agc acc	159
	Thr Arg Lys Lys Pro Arg Val His Gln Arg Pro Ala Pro Gln Ser Thr	
	15 20 25	
	agg gtg ggg gtc tcc tcc gaa gca aga tat gaa acc ctt tca gtg ctt	207
15	Arg Val Gly Val Ser Ser Glu Ala Arg Tyr Glu Thr Leu Ser Val Leu	
	30 35 40	
	gct ctg agc agc tca gaa gta gaa tgc gag agg acc tca ctg ttc tga	255
	Ala Leu Ser Ser Ser Glu Val Glu Cys Glu Arg Thr Ser Leu Phe *	
20	45 50 55	
	cgatgattgt ccaacacaca tccggccctc tccgtgtctc ctcccaccac catcttctcc	315
	tatcaccggg cttactatct tctctcctgg ctttcctctt tctgatggcg gttcctgaag	375
	cctccaacta acccctaact cggggagcgc ctcgacagtg tttgtggcta aggctacact	435
25	cagagacaga gttgcagaat gagggagacc cagcccaggg gacgccattg ctgggaggta	495
	gactgggtgc gagggccctt ggcacaggac tcacatctgg gctgttcagc ttgacccgaa	555
	ggctgtgtgt gaaaggggga aaaagacaag attgccaggc agggctgttg tttttgtggc	615
	ttcgagggac aagaacctgg ctaaaaggca gcagccctgc tgttcttttt ctctctgtc	675
	ctgtttccta ccttacaaga agtccatgca accaaccggg gctctggcac ttttctgtt	735
30	tatttccctc ctggcttcca aacaagccct ctgtggacat catcaaagea tggataacct	795
	cctctgcagg ggtgggcttc attctccgct ggtccctgta gccttcctgg acacagggtg	855
	aaagttgtaa aagtggtagg agtgcagcta gccacagggt ctccttttcc catctcagtc	915
	tgaccaagga ggctgaacta ccaacccaaa ttcagcgaaa aaaaaaaaaa aaaaaaaaaa	975
35	aagcggccgc	985
40		
45		
50		
55		

FIGURE 29

5	tctagcgaac cccttcgcgg ggacagacat ggagaaggag atggaggacc ccctggctgg	60
	agcagaccaa cagaataggc aactatggct ggagaaccgg gtatcagagt aatgcttgac	120
	ctcgggaaac accaaatttc ttcttccgat cgcagaagta gtactcggcg aaattcacta	180
	ggtaggaggc tcctcatctg ggaagaaccg gtgcctgggg ggacctggct ggataggt	238
	atg ggg gat cga ggc cgg tcc cct agt ctc cgg tcc ccc cat ggc agt	286
10	<u>Met Gly Asp Arg Gly Ser Pro Ser Leu Arg Ser Pro His Gly Ser</u>	
	<u>-35 -30 -25 -20</u>	
	cct cca act cta agc acc ctc act ctc ctg ctg ctc ctc tgt gga cag	334
15	<u>Pro Pro Thr Leu Ser Thr Leu Thr Leu Leu Leu Leu Leu Cys Gly Gln</u>	
	<u>-15 -10 -5</u>	
	gct cac tcc cag tgc aag atc ctc cgc tgc aat gcc gag tac gtc tcg	382
	<u>Ala His Ser Gln Cys Lys Ile Leu Arg Cys Asn Ala Glu Tyr Val Ser</u>	
	<u>1 5 10</u>	
20	tcc act ctg agc ctt cgg gga ggg ggc tca ccg gac acg cca cat gga	430
	<u>Ser Thr Leu Ser Leu Arg Gly Gly Gly Ser Pro Asp Thr Pro His Gly</u>	
	<u>15 20 25</u>	
25	ggc ggc cgt ggt ggg ccg gcc tca ggt ggc ttg tgt cgc gcc ctg cgc	478
	<u>Gly Gly Arg Gly Gly Pro Ala Ser Gly Gly Leu Cys Arg Ala Leu Arg</u>	
	<u>30 35 40 45</u>	
30	tcc tac gct ctc tgc acg cgg cgc acc gcc cgc acc tgc cgc ggg gac	526
	<u>Ser Tyr Ala Leu Cys Thr Arg Arg Thr Ala Arg Thr Cys Arg Gly Asp</u>	
	<u>50 55 60</u>	
35	ctc gct ttc cac tcc gcg gtg cat ggc ata gag gac ctg atg atc cag	574
	<u>Leu Ala Phe His Ser Ala Val His Gly Ile Glu Asp Leu Met Ile Gln</u>	
	<u>65 70 75</u>	
	cac aac tgc tca cgc cag ggt ccc acg gcc tcg ccc ccg gcc cgg ggt	622
	<u>His Asn Cys Ser Arg Gln Gly Pro Thr Ala Ser Pro Pro Ala Arg Gly</u>	
	<u>80 85 90</u>	
40	cct gcc ctg ccc ggg gcc ggc cca gcg ccc ctg acc cca gat ccc tgt	670
	<u>Pro Ala Leu Pro Gly Ala Gly Pro Ala Pro Leu Thr Pro Asp Pro Cys</u>	
	<u>95 100 105</u>	
45	gac tat gaa gcc cgg ttt tcc agg ctg cac ggt cga acc ccg ggt ttc	718
	<u>Asp Tyr Glu Ala Arg Phe Ser Arg Leu His Gly Arg Thr Pro Gly Phe</u>	
	<u>110 115 120 125</u>	
50	ttg cat tgt gct tcc ttt gga gac ccc cat gtg cgc agc ttc cac aat	766
	<u>Leu His Cys Ala Ser Phe Gly Asp Pro His Val Arg Ser Phe His Asn</u>	
	<u>130 135 140</u>	
55	cac ttt cac aca tgc cgc gtc caa gga gct tgg ccc cta cta gat aac	814
	<u>His Phe His Thr Cys Arg Val Gln Gly Ala Trp Pro Leu Leu Asp Asn</u>	
	<u>145 150 155</u>	
	gac ttc ctc ttt gtc caa gcc acc agc tcc ccg gta gca tcg gga gcc	862

Downloaded from www.jstor.org

Asp Phe Leu Phe Val Gln Ala Thr Ser Ser Pro Val Ala Ser Gly Ala
 160 165 170

FIGURE 29 (cont.)

5	aac gct acc acc atc cgg aag atc act atc ata ttt aaa aac atg cag	910
	Asn Ala Thr Thr Ile Arg Lys Ile Thr Ile Ile Phe Lys Asn Met Gln	
	175 180 185	
10	gaa tgc att gac cag aaa gtc tac cag gct gag gta gac aat ctt cct	958
	Glu Cys Ile Asp Gln Lys Val Tyr Gln Ala Glu Val Asp Asn Leu Pro	
	190 195 200 205	
15	gca gcc ttt gaa gat ggt tct gtc aat ggg ggc gac cga cct ggg ggc	1006
	Ala Ala Phe Glu Asp Gly Ser Val Asn Gly Gly Asp Arg Pro Gly Gly	
	210 215 220	
20	tcg agt ttg tcc att caa act gct aac ctt ggg agc cac gtg gag att	1054
	Ser Ser Leu Ser Ile Gln Thr Ala Asn Leu Gly Ser His Val Glu Ile	
	225 230 235	
25	cga gct gcc tac att gga aca act ata atc gtt cgt cag aca gct gga	1102
	Arg Ala Ala Tyr Ile Gly Thr Thr Ile Ile Val Arg Gln Thr Ala Gly	
	240 245 250	
30	cag ctc tcc ttc tcc atc agg gta gcg gag gat gtg gca cgg gcc ttc	1150
	Gln Leu Ser Phe Ser Ile Arg Val Ala Glu Asp Val Ala Arg Ala Phe	
	255 260 265	
35	tct gct gag cag gat cta cag ctg tgt gtt ggg gga tgc cct ccg agc	1198
	Ser Ala Glu Gln Asp Leu Gln Leu Cys Val Gly Gly Cys Pro Pro Ser	
	270 275 280 285	
40	cag cga ctc tct cgc tca gag cgc aat cgc cgt ggg gcg ata gcc ata	1246
	Gln Arg Leu Ser Arg Ser Glu Arg Asn Arg Arg Gly Ala Ile Ala Ile	
	290 295 300	
45	gat act gcc aga agg ttg tgt aag gaa ggg ctt ccg gtt gaa gat gcc	1294
	Asp Thr Ala Arg Arg Leu Cys Lys Glu Gly Leu Pro Val Glu Asp Ala	
	305 310 315	
50	tac ttc caa tcc tgc gtc ttt gat gtt tca gtc tcc ggt gac ccc aac	1342
	Tyr Phe Gln Ser Cys Val Phe Asp Val Ser Val Ser Gly Asp Pro Asn	
	320 325 330	
55	ttt act gtg gca gct cag tca gct ctg gac gat gcc cga gtc ttc ttg	1390
	Phe Thr Val Ala Ala Gln Ser Ala Leu Asp Asp Ala Arg Val Phe Leu	
	335 340 345	
60	acc gat ttg gag aac ttg cac ctt ttc cca gta gat gcg ggg cct ccc	1438
	Thr Asp Leu Glu Asn Leu His Leu Phe Pro Val Asp Ala Gly Pro Pro	
	350 355 360 365	
65	ctc tct cca gcc acc tgc cta gtc cgg ctt ctt tcg gtc ctc ttt gtt	1486
	Leu Ser Pro Ala Thr Cys Leu Val Arg Leu Leu Ser Val Leu Phe Val	
	370 375 380	
70	ctg tgg ttt tgc att cag taa gtaggccagc aaccctgtgac tagttttggaa	1537

Leu Trp Phe Cys Ile Gln *

385

FIGURE 29 (cont.)

5	acggtttgag	gagagagggt	gatgtgagaa	aacacaaaaga	tgtgccaaaag	gaaacagtgg	1597
	ggacaggaga	caacgacctt	actcaatcac	acgagggtgc	agtccagggc	tgaaatgacc	1657
	ctagaataaa	gattctgaga	caggggtttg	cactccagac	cttggtatgg	gctcccatg	1717
	aatttcccca	ttagtgattt	cccacttgta	gtgaaattct	actctctgta	cacctgatat	1777
	cactcctgca	aggctagaga	ttgtgagagc	gctaagggcc	agcaaaacat	taaagggctg	1837
10	agatatctta	aaggcagaaa	ctagaaaagg	ggaaaccatg	attatctata	agaaaatcaa	1897
	aagagggggt	tgggaattta	gctcagtggg	agagcacttg	cctagcaagc	gcaaggccct	1957
	gggttcggtc	cccagctcct	aaaaaaaaaa	aaaaaaaaaa	aaaaagcggc	cgc	2010

15

20

25

30

35

40

45

50

55

FIGURE 30

5	tctagcgaac cccttcgtgg ggattaaggt tctctatagc taagcctgtc nga atg	56
	Met	
	1	
10	aca aca ccc aga gat ctc acc tgg ggt ggt ggg agc act ctc tgt ctt	104
	Thr Thr Pro Arg Asp Leu Thr Trp Gly Gly Gly Ser Thr Leu Cys Leu	
	5 10 15	
15	gag gga aca tgt acc tac tct ctc ctt cca caa gag cca cat aca ctt	152
	Glu Gly Thr Cys Thr Tyr Ser Leu Leu Pro Gln Glu Pro His Thr Leu	
	20 25 30	
20	aga agt tcc agt gaa gat cta tgt gct tca gaa gag agg gga ctt gga	200
	Arg Ser Ser Ser Glu Asp Leu Cys Ala Ser Glu Glu Arg Gly Leu Gly	
	35 40 45	
25	ggt gaa agg ggg agt ggg agg ggg gct tga ggacctanct gaaagatttt	250
	Gly Glu Arg Gly Ser Gly Arg Gly Ala *	
	50 55	
30	angctgaaaag aacttccttg attcaaagac atatgtcagt ngaccaaca atgagaatga	310
	atatgagggc caggaaaact tgtgggaatc agtctcaaga cngaaacnga gaaagaaaga	370
	aaagtggnta ggactcanat tggggaacct gggtagacag gagtggcnag ggaagaaagg	430
	gatcttgggt tntccacagt ttgagacaca tccgngntc gacctattc ccngaagecn	490
	cannanatgt tgcttcccn tcnntnnaat gggcctggng gtectnctcc ctttncnng	550
35	gacatgaaaa ngtnnctgc nnanataacc cccntctttc ctcccccttn antntgtccc	610
	taccnttttg tccctttttn ttttnaaaaa annaaaaataa aggggnncnn tnttcccttn	670
	gaaaaaaaaa aaaaaaaaaa aaaaaaccgc ccncc	705
40		
45		
50		
55		

FIGURE 31

5	tctagcgaac cccttcgcga aggggttcgc ttacattcac gcttaagcat attaaactgta	60
	catattaact gatttagagg atact atg gat tcc aca tct tcc ctg agc ata	112
	Met Asp Ser Thr Ser Ser Leu Ser Ile	
	1 5	
10	ggg att gat ttg aaa aat gac agg gtt ggc tgt cga ccc cca tcg gag	160
	Gly Ile Asp Leu Lys Asn Asp Arg Val Gly Cys Arg Pro Pro Ser Glu	
	10 15 20 25	
	gaa gca ggt aag gaa tca ctt agg aga act gat ctc aac att ctt cag	208
15	Glu Ala Gly Lys Glu Ser Leu Arg Arg Thr Asp Leu Asn Ile Leu Gln	
	30 35 40	
	ttc ttt cta tta ttt act tgt tta gcc tgg agt taa attcccactc	254
	Phe Phe Leu Leu Phe Thr Cys Leu Ala Trp Ser *	
20	45 50	
	cttgtgagca cttctaattt gaaaatccac tttcttcaat attttcgaaa tttaaaactg	314
	atggatgacg tgacaaaact tccacgagtt aagaattctc cacctctgat ctcatcgag	374
	cagggcacia tccaaggcat gtgaattgac ttccagggtt atgtgacata taaatgaatt	434
25	ctgtctctag atttgatcc cattctccta aatatctcac catgcatgtg cagatattct	494
	aaagtctaaa aatatctgat attgcaaact tttctggtca aaacattttg gatgagccat	554
	ttaacagcca aggtatttga gacagagggt tcaacagcat tcctggagga gacacaaagg	614
	acagatgagt cacatgaagg atgggaggag ggaagggtggc tgttgatagg tatttttgaga	674
	cactctattt gagtcctaca caacactccc cctccccccc ctccccccaa accatttttta	734
30	tgtctattga cctttcctct agtcatacag ggacattcac agttacctac aaagaaccag	794
	aattgtaaca agtcaagagg aaacttattt ttgataatga ctcatggaag atgttttgaa	854
	aatttaaaaa taagctcttg taagcagaag tctgtgagaa aagcaagaag gaattgtttg	914
	tttattaaat aaataaaaagg cnnannnnnaa aaaaaaaaaa aaaaangcgg ccgc	968
35		
40		
45		
50		
55		

FIGURE 32

5	tctagcgaac cccttcggca gacagcatcc ctcccaaggc tactcagggt ttaaaccctg	60
	cttctgaagt gacatgtcct gcaaagaaag tccccacgtg ggtgtttcca ccaccactgt	120
	cagctctgta gctgtgcaag ctgggggactc caagatcgtg atagccgttg tcaagtgtgg	180
	caaatgggtg cggtccaac tggctgaggc acagcccaat ctccctagaaa ttgggagcag	240
	tcaag atg aaa cca gaa aac tgc ttc acg atc acg agc tcc ttc tgg cca	290
10	Met Lys Pro Glu Asn Cys Phe Thr Ile Thr Ser Ser Phe Trp Pro	
	1 5 10 15	
	agc tta agg cct tgg aag atc gtg tgt ggg gac tct tac agg aag cag	338
	Ser Leu Arg Pro Trp Lys Ile Val Cys Gly Asp Ser Tyr Arg Lys Gln	
15	20 25 30	
	aca gga cgg ctg aag caa aca agg agc aaa gtg agg tgt cga tgc cat	386
	Thr Gly Arg Leu Lys Gln Thr Arg Ser Lys Val Arg Cys Arg Cys His	
	35 40 45	
20	ggc cag act ctg ggc gaa gca tgg gcc acc ctg gtc ttc atg ctt gaa	434
	Gly Gln Thr Leu Gly Glu Ala Trp Ala Thr Leu Val Phe Met Leu Glu	
	50 55 60	
25	aga aga agg gag ctc ctc gga ctg aca tct gag ttt ttt caa agc gcc	482
	Arg Arg Arg Glu Leu Leu Gly Leu Thr Ser Glu Phe Phe Gln Ser Ala	
	65 70 75	
30	ttg gag ttt gct ata aaa ata gac caa gct gaa gat ttt ctg cag aat	530
	Leu Glu Phe Ala Ile Lys Ile Asp Gln Ala Glu Asp Phe Leu Gln Asn	
	80 85 90 95	
35	cct cac gag ttt gag agt gcc gaa gcc tta cag tca ctt ctt ctg ctt	578
	Pro His Glu Phe Glu Ser Ala Glu Ala Leu Gln Ser Leu Leu Leu Leu	
	100 105 110	
	cat gac cga cac gcc aaa gaa ctc tta gaa cga tct cta gtc ctt tta	626
	His Asp Arg His Ala Lys Glu Leu Leu Glu Arg Ser Leu Val Leu Leu	
	115 120 125	
40	aac aaa agc caa caa ctc act gac ttc ata gaa aaa ttc aag tgt gat	674
	Asn Lys Ser Gln Gln Leu Thr Asp Phe Ile Glu Lys Phe Lys Cys Asp	
	130 135 140	
45	gga tct cct gtg aat tct gag ctc atc cag gga gct cag agc agt tgt	722
	Gly Ser Pro Val Asn Ser Glu Leu Ile Gln Gly Ala Gln Ser Ser Cys	
	145 150 155	
50	ctg aag atc gac agc ctc ctt gaa ctt ctg caa gac agg aga agg cag	770
	Leu Lys Ile Asp Ser Leu Leu Glu Leu Leu Asp Arg Arg Arg Gln	
	160 165 170 175	
55	ctg gac aag cac ttg cag caa cag agg cag gag ttg tct cag gtt ctg	818
	Leu Asp Lys His Leu Gln Gln Gln Arg Gln Glu Leu Ser Gln Val Leu	
	180 185 190	
	cag tta tgt ctg tgg gac caa caa gaa agc cag gtt tct tgt tgg ttt	866

Gln Leu Cys Leu Trp Asp Gln Gln Glu Ser Gln Val Ser Cys Trp Phe
 195 200 205

FIGURE 32 (cont.)

5	cag aaa aca ata aga gat ctg cag gaa cag agt ctg ggt tca tcc ctt	914
	Gln Lys Thr Ile Arg Asp Leu Gln Glu Gln Ser Leu Gly Ser Ser Leu	
	210 215 220	
10	tca gac aac aaa gag tta atc cgt aag cac gag gac ctg cca tca aag	962
	Ser Asp Asn Lys Glu Leu Ile Arg Lys His Glu Asp Leu Pro Ser Lys	
	225 230 235	
15	caa aga gtc cct gca gtt tag gaattgaaca gaacagtttc ctgattgaat	1013
	Gln Arg Val Pro Ala Val *	
	240 245	
20	gatcttggcg cctyyttanc ggntgcagat ggtggggcct cctctggntt ctcatectct	1073
	tccactaatc tggatttttg ttcccttggt gtgccacatc actttaattt gaaagaaaaa	1133
	aaataaattg ggccggaaaa aaaaaaaaaa aaaaaaaaaa rrscggccnc	1183
25		
30		
35		
40		
45		
50		
55		

FIGURE 33

5	tctagcgaac	cccttcgcg	aagatggccg	cttcccagac	cgctccgcg	catcttcaag	60
	atgcgcgaga	agaacgtgca	atctcgcgag	atcaggctcg	ctcgcgggca	gtctgctcgc	120
	agcctaccct	tcctaggagt	tggaggagg	aaagctagat	tcgattaaga	gcaaaaaatt	180
	gttccagcag	cagagcagct	gtccaaggaa	gtatccaaag	gaactgcacc	tcagtaaact	240
	cctggcaagt	cttaggatat	gacaaagggc	acaggatgca	ttatgagaaa	ggaaggctaa	300
10	ggttttcaag	aacacagatt	tacatcaaac	ttgcgttctg	aattaatctt	tgagaatact	360
	ggactgtgag	ctagacattg	agtaagaggt	ttgttatatc	aagaatgtga	tctaaaaaaaa	420
	aaacattcat	atcttcctcc	cacaagagga	tattttgaaa	ctgtgggtca	aagtcagact	480
	acaggagagc	cctcaaatat	gccaaatgtg	acagacagca	ggattttgaa	aatatagtgg	540
	gagtatgtga	agatgttcca	gtcaaagaga	cattgtttcc	aaaggaaaga	aagtccagtc	600
15	gcctcacagg	aattgtgtat	tccctggtag	taatgcaa	ggaccacata	tggctttctt	660
	ctttaaagag	aataccta	tttagctaca	gagtataatg	ctgatgatac	aaaccgtgac	720
	aagtggagg	acaagaaagt	aaatggactg	atggtgccat	tgtggactgg	gagggtaaaa	780
	gctgtacatt	tgtgaacaaa	aagatttcct	tgttatggtc	agccatgatt	ctaactgcta	840
	aatggaggca	gtaacaacat	gacctaaaga	gtaaacatcc	agagatggaa	tgttctcaat	900
20	gtctgaaaag	gagcagatat	ctgggtgatg	tgaatgatg	ctagagattt	tttacaagcc	960
	tgtggtgaat	tagtaattgt	attttatttt	gaaagttaa	caggtaatta	gaaaccccaa	1020
	aaaaaaaaa	aataaaaaa	aagcgccgc	c			1051

25

30

35

40

45

50

55

FIGURE 34

5	tctagcgaac	cccttcgctg	aaaccaccgt	tcacacggga	aacctggggt	aggcttttgt	60
	cctcagtgac	acagaggatg	tagtccacag	ctaggtagaa	atgtcagggt	cccaacacta	120
	ctccagctgt	gactttgatg	cttgggggat	ggggtcgcag	gctattttct	ctgctttaac	180
	agttcataga	atttaacaga	taagagttag	tgtctttcat	gtggcctcac	tctggagtta	240
	tgagaacata	cacacgggtt	acagcttttc	aatatncctt	tccctggcca	tcaagtattt	300
10	tgaaagtgtg	ccacctttta	acctttgcgc	tttatttttt	tttctttttt	taaagntgaa	360
	ggtgataatt	cttctatata	tgatgaaact	caatgtctac	tgaaataagt	gtaaccttag	420
	ctatncacgt	ttatntttta	aaaccacgct	atggagatat	taccccgagt	tctgtcnttt	480
	ngcaagattt	acagnacctt	ccncccccc	cttttagcat	tnaataaaaa	natattgggg	540
	agcncnntna	aaaaaaaaa	aatnaanaaa	agcggc			576

15

20

25

30

35

40

45

50

55

FIGURE 35

5	tctagcgaac cccttcgcgt gatctgatcc gagctgagac ttggggagct ctggctccgt	60
	gttggctgca gcatcccca tggctctgtc tgaggtgtcc tgtgactcga ctcttcagaa	120
	ctcaatgaag tagatgactt gactacaatg tggaaacatc atg aca gaa agt gtg	175
	Met Thr Glu Ser Val	
	1 5	
10	gtt tgt acc ggg gcc gtc agc act gta aag gaa gtc tgg gaa gaa aga	223
	Val Cys Thr Gly Ala Val Ser Thr Val Lys Glu Val Trp Glu Glu Arg	
	10 15 20	
15	ata aag aaa cat cat gaa gat gtg aaa cga gag aag gaa ttt cag caa	271
	Ile Lys Lys His His Glu Asp Val Lys Arg Glu Lys Glu Phe Gln Gln	
	25 30 35	
20	aag cta gtg cgg atc tgg gaa gac cga gtg agt tta act aag ctg aaa	319
	Lys Leu Val Arg Ile Trp Glu Asp Arg Val Ser Leu Thr Lys Leu Lys	
	40 45 50	
25	gag aag gtg acc agg gaa gat gga aga atc att cta agg ata gag aaa	367
	Glu Lys Val Thr Arg Glu Asp Gly Arg Ile Ile Leu Arg Ile Glu Lys	
	55 60 65	
30	gag gaa tgg aag act ctc cct tct tcc tta ctg aaa ctg aat cag cta	415
	Glu Glu Trp Lys Thr Leu Pro Ser Ser Leu Leu Lys Leu Asn Gln Leu	
	70 75 80 85	
35	cag gag tgg caa ctt cat agg acc gga ttg ttg aaa att cct gaa ttc	463
	Gln Glu Trp Gln Leu His Arg Thr Gly Leu Leu Lys Ile Pro Glu Phe	
	90 95 100	
40	att gga aga ttc cag cat ctc att ggt cta gac tta tct cgg aac aca	511
	Ile Gly Arg Phe Gln His Leu Ile Gly Leu Asp Leu Ser Arg Asn Thr	
	105 110 115	
45	att tca gag atc ccc ccg agg cat tgg act gnt cac tta gac ttc aag	559
	Ile Ser Glu Ile Pro Pro Arg His Trp Thr Xaa His Leu Asp Phe Lys	
	120 125 130	
50	gaa ctg att ctt agc tac aca aaa tca a	587
	Glu Leu Ile Leu Ser Tyr Thr Lys Ser	
	135 140	

FIGURE 36

5	tctagcgaac	cccttcggtt	ctgttggcta	cacagctgca	gagccatggc	tgaccgttca	60
	ctgtcagggg	cacatgttac	actaagcttc	atgacagtga	tgtaataatg	ttacacattt	120
	gtcttgtagt	tatgtattga	agtttctgtc	ctgttttgtg	taaaaatgta	tccactcttg	180
	tatatattta	gacttgaaac	taccacacaa	atattggaac	ggtttgcttt	atgaagttaa	240
	aagtatcctt	ccgaatggaa	ctaacttgct	ttgtgctcag	acataacta	tgctgatgta	300
10	ttttgcaata	tactatctta	aattaaatct	ggtcactttg	ttgccttttt	aaaaagtgtg	360
	gtatttcaag	tagagttatt	ttcctgaaat	atatttgcaa	actcaagctg	ctttataatc	420
	aaggaatatt	tttattgatt	gaagaaaatg	actgctgcaa	ttcaaaaagt	aacttatttt	480
	attatataga	tgatttctta	aaagctattt	ataccatgat	acaaaatcat	gtagtgatcc	540
	tgggagtctg	tagttcttcc	tgtaataaac	attcaacact	gtatgctaga	ggcagcaatg	600
15	ccaacactga	agttattttg	ggtgaaaacc	gtcgttctgn	cctgttttagc	tggggattat	660
	taaatccata	taatgtatgt	gcttatgtat	gctacatgtg	caagttaggt	gtttcctttg	720
	tgttctgctt	attaaatgtc	attcagattc	acttctgtaa	ttctaataaa	gaggggaagct	780
	attggaaaaa	ataaaaaaaaa	aaaaaaaaaaa	gcggccgcc			819

20

25

30

35

40

45

50

55

FIGURE 37

5	tctagcgaac	cccttcggtg	gcgcacgccg	gtaggatttg	ccacgcaa	gctggaatta	60
	aagacatgca	gcagcagcgc	cctgtgggtt	tgggttttta	tttgattgct	tattttttatc	120
	taatttttaa	ttttttgtgt	atgaacgttt	tatctgcatt	tatgtctctg	taccacattc	180
	gtgcctggtg	ctatggaggc	caaaaaagga	ttttaggccc	gagattgtag	ttatagatgg	240
	ttgtgggctg	ccaatctgag	tgctgaaaat	taaacctggg	tactctgaaa	gaccagccag	300
10	tgctcttaac	tatcaggcca	cctctccagc	actattttat	tttattttat	ttgtggagat	360
	agggctcttc	tctctgtatc	ctagtctaac	ttaaaacata	aagaatattc	tgtatcagta	420
	tccttgagta	ctaggattct	aggcacctgt	cattatgcct	agatttttaa	cagtgtgtgt	480
	taattctaca	taaaaatgaa	tttcattatt	acattttcac	acttgtgaag	aataactttt	540
	gatcatattc	ccttctcctg	atactttttc	ctatccttcc	tccccactcc	attagttccc	600
15	ttcttctttt	cagagtctac	cttctacttt	ttactttgat	ttttttcccc	ccacattctg	660
	tggttgagag	aatgcatatt	acagttgtat	ttctgaatct	ggctaggtac	attcacttaa	720
	cataattaat	gatcctgggc	gagcgaaggg	gttcncctan	cnaacccctt	cggttcaata	780
	ccatttcaga	gatgggcatt	tccttcaatg	aaatacacaa	gtaaacattc	cgacattgtc	840
	tttaggagtg	tttgttaaaa	aaaaaaaaaa	aaaaaaccan	anccccaaan	caaaaaaaaaa	900
20	aaagctttgc	accttgcaaa	agtggtcctg	gcgtgggtag	attgctgtta	atcctttatc	960
	aataacgttc	tatagagaat	atataaatat	atatataatt	atatctccta	gtccctgcct	1020
	cttaagagcc	gaaaatgcat	gggtgttgta	gacattcggg	tgactaaat	tcctctctga	1080
	attttggctg	ctgaagccgt	tcatttagca	actgtttata	gggtggtgat	gaatggttcc	1140
	ttatctccat	ttcttcctat	gtagcttaag	ccgcttcctt	cacagaatct	aataatctcg	1200
25	tctaggccat	tagccctgcc	ctttcttaac	attcttgtat	ttgttgaatt	tggcctcctc	1260
	gaaagcaata	gcaactgggt	ggcccaccca	agttttaacg	cccctgattc	catctatggc	1320
	atttgtacca	aatataagtt	ggatgcattt	attttagaca	caaagcttta	ttttttcgac	1380
	atcgtgtttc	aagaaaaaaaa	acaaatagaa	taacaataac	tatgactttg	aggccaatca	1440
	tttttaggtg	tgtgtttgaa	gcatagaacg	tctnttaa	tctcaatggg	tccttcaaat	1500
30	gatgagttag	tatgtaacgt	aaatagcagt	ttctctctct	ctctctctct	ttttattttt	1560
	tccanataga	gcactatgta	aatttagcat	atcaataata	caggaactat	ccnccaaaaa	1620
	aaaaaaaaaa	aaaaaaaaaa	gcggccgc				1648

35

40

45

50

55

FIGURE 38

5	tctagcgaac	cccttcgtag	aactaggagc	cagtgttgac	cacggtcggt	ggctggatac	60
	cccactgcat	gctgcagcaa	ggcagtcag	tgtggaggtc	atcaatctgc	tcactgagta	120
	tggggctaac	ctgaaactca	gaaactcgca	gggcaaaagt	gctcttgagc	tcgctgctcc	180
	caaaagtagt	gtggagcagg	cactcctgct	ccatgaaggt	ccacctgctc	tttctcagct	240
	ctgccgcttg	tgtgtccgga	agtgtctggg	ccgcac atg	tca tca agc	cat cta	294
10				Met	Ser Ser Ser	His Leu	
				1		5	
	cgc act agg	tct gcc aga	acc cct gga	aaa att cct	ctt ata cca	ata	342
	Arg Thr Arg	Ser Ala Arg	Thr Pro Gly	Lys Ile Pro	Leu Ile Pro	Ile	
15		10		15		20	
	gtt gga aac	atg ttg cct	gct gta gga	cac tta ata	tac aca ttc	agt	390
	Val Gly Asn	Met Leu Pro	Ala Val Gly	His Leu Ile	Tyr Thr Phe	Ser	
		25		30		35	
20	ggc tta acc	cac tat cct	aaa aat ctg	ctt acc taa	ttagaataaa		436
	Gly Leu Thr	His Tyr Pro	Lys Asn Leu	Leu Thr *			
		40		45			
25	gccttcataa	atccaaatac	ttgcgttgaa	caaactcctg	gttaggttaa	tggntgccaa	496
	gagataacca	gaaacctttc	aagtttttaa	ctcttggtaa	tttaaaatca	aactgaaata	556
	gatggaaaaat	aataatctat	ttttggataa	ttcaaggacc	cttcagtatc	tggggctggg	616
	gtccgcattt	tgnatactgg	atagacacac	acacaggtag	gatanggtaa	atnaactact	676
	taaagaatgg	cctgggattt	aagtcctcca	gatatttttt	aggtngnggt	ttcctaaaat	736
30	aaaattctgg	agtgccaaaa	aaaaaaaaaa	aaaaaaaaag	cgggcc		782
35							
40							
45							
50							
55							

FIGURE 39

5	gtctagcgaa ccccttcggg aaacttcaac aaaggtacca gcaactacag cgccttgtcc	60
	acccagattt cttcagccaa aagtctcaga ctgagaaacg gttctcggag aagcattcga	120
	ccctgggtgaa tgatgcctac aagactcttc aggcccccgt gagcagagga ctatatcttc	180
	taaagctcca aggaatagaa attcctgaag ggacagatta tagaacagac agtcagttcc	240
	ttgtggaaat c atg gaa atc aat gaa aaa ctc gca gac gcc aaa agt gag	290
10	Met Glu Ile Asn Glu Lys Leu Ala Asp Ala Lys Ser Glu	
	1 5 10	
	gca gcc atg gaa gag gta gaa gcc act gtc aga gct aaa cag aaa gaa	338
	Ala Ala Met Glu Glu Val Glu Ala Thr Val Arg Ala Lys Gln Lys Glu	
15	15 20 25	
	ttt acg gac aat ata aac aga gct ttt gaa caa ggt gat ttt gaa aaa	386
	Phe Thr Asp Asn Ile Asn Arg Ala Phe Glu Gln Gly Asp Phe Glu Lys	
	30 35 40 45	
20	gcc aag gaa ctt ctt aca aaa atg aga tac ttt tca aac ata gaa gaa	434
	Ala Lys Glu Leu Leu Thr Lys Met Arg Tyr Phe Ser Asn Ile Glu Glu	
	50 55 60	
25	aag atc aag tta agc aag aac cct ctc tag ttgctaactt aaaggtttaa	484
	Lys Ile Lys Leu Ser Lys Asn Pro Leu *	
	65 70	
30	aaataaaactt tgtattttctt cannnnnnnan nnnnnannntn nnnnagcggc cgcc	538
35		
40		
45		
50		
55		

FIGURE 40

5	tctagcgaac	cccttcgcga	aggggttcgc	ttcttaccct	gtggagaaaag	gggcaggagg	60
	aacctcctgt	gttaggagga	agctggagct	taccactgtg	agaggacaga	tgtggactga	120
	gaatthttctt	agtgtctcagt	ggcacttccc	aaggactccc	ctccccttgt	gctctgtgcg	180
	gttttttagga	cagctaagat	gactgccacc	tgttgtggca	ggcccgattt	gtcttgttct	240
	ccccttactg	taccccgata	taatctctgt	tgatcaacag	gactacccca	agaatccaca	300
10	tgttctcccc	cgtaaccagg	cagctgtctg	gttcatgcct	tcttcccttc	aaaccacaacc	360
	cagcgccctt	gttagtgaag	aggtggtcca	tggtactgatg	acaagtattt	agcactggat	420
	gctgtttcca	tagtgacaag	cctatacctc	ttcccaccct	ttagtgcgca	gtgggctgct	480
	gcttcagtat	cctcccagct	cagttttatt	agatcaaagc	tgcccttggg	caccatgttg	540
	gccacctcaa	tcaccagcca	aaatggtcgc	tttgtccacc	agaggtcaag	ccatctttct	600
15	ggcgtgtag	ttcccagctc	cttctagggg	acaggaagtt	gatattgccg	tgggggaggt	660
	ggcgggggtg	ggccgtcacc	tcaatagttt	tactgtaaaa	gggaaatttg	aacaagaaca	720
	acaacaaaaa	aaaaaaaaaa	acaaagaaaa	aaataaaaaa	ctttaaaaagt	tgaaaaaaaa	780
	aaaaaaaaaa	aaaaaaagcg	gccgc				805

20
25
30
35
40
45
50
55

FIGURE 41

5	tctagcgaac cccttcgctg ggacccgcaa ctaccaactg ccgcctggat cctaggtgag	60
	ctgtgggctc tgacagcgct gtggctaac atg gca ccc aaa aag aag act ctc	113
	Met Ala Pro Lys Lys Lys Thr Leu	
	1 5	
10	aag aag aac aaa ccc gag atc aat gag atg acc atc atc gtg gaa gac	161
	Lys Lys Asn Lys Pro Glu Ile Asn Glu Met Thr Ile Ile Val Glu Asp	
	10 15 20	
	agc ccc cta aac aag ctg aat gct cta aat ggg ctc ctg ggg gga gaa	209
15	Ser Pro Leu Asn Lys Leu Asn Ala Leu Asn Gly Leu Leu Gly Gly Glu	
	25 30 35 40	
	aac agc ctt agc tgt gtt tct ttc gaa cta aca gac act tct tat ggt	257
	Asn Ser Leu Ser Cys Val Ser Phe Glu Leu Thr Asp Thr Ser Tyr Gly	
20	45 50 55	
	ccc aac ctc ctg gaa ggt tta agt aaa atg cgt caa gag agc ttt cta	305
	Pro Asn Leu Leu Glu Gly Leu Ser Lys Met Arg Gln Glu Ser Phe Leu	
	60 65 70	
25	tgt gac ttg gtc atc ggt cca aaa cca agt cct ttg atg tcc ata agt	353
	Cys Asp Leu Val Ile Gly Pro Lys Pro Ser Pro Leu Met Ser Ile Ser	
	75 80 85	
30	caa gtg atg gct tcc tgc agc gag tct tct ata ata tcc tta aaa cga	401
	Gln Val Met Ala Ser Cys Ser Glu Ser Ser Ile Ile Ser Leu Lys Arg	
	90 95 100	
	tcc atc gac aaa aag ggt aga cct caa tga tatcgnccct ttagggctac	451
35	Ser Ile Asp Lys Lys Gly Arg Pro Gln *	
	105 110	
	caccgtgata gcatatgcat acacnggaaa gctgcccttt ctttatacac aataaggaag	511
	catcatttct gctgctgtgt acctccagat ccacactctt gtgaagatgt gcagcgactt	571
40	tctgatccga gagatcagt ttgagaactg catgtatgtt gttaacatgg ctgaaacata	631
	ctgcttgaaa aatgcgaaag caacggccca gaaatttatc cgggataact tcattgaatt	691
	tgccgactcc gaacaattta tgaagctgac gtttgaacag attaatgagc ttctcataga	751
	tgatgacttg cagttgcctt ctgagctggt agcattccag attgcaatga aatggataga	811
	attcaaccaa aagagagtga agcacgctgc ggatctttta agcaatattc gctttggtac	871
45	catctctgca caagacctgg tcaattacgt tcaaaccgta ccgagaatga tgcaagacgc	931
	tgattgtcat aaactgcttg tggatgctat gaactaccac ttactacctt atcatcaaaa	991
	cacgttgcaa tctaggcgga caagaattag aggcggctgc cgggttctga tcaactgtcg	1051
	gggacgccct ggctgactg agaagtccct tagtagagac gtttatatag agaccctgaa	1111
	aatggatgga gcaagcttac agaaatgccca gccaaagagt tcaatcagtg tgtggctgtg	1171
50	atggatggat tcctttatgt agcaggtggt gaggaccaga atgatgagc aaaccaagcc	1231
	aagcatgcag tcagcaattt ctgcaggtac cgatccccgc ttcaacacgt ggatccacct	1291
	gggcagcatg aaccagaagc gcacgcactt cagcctgagc gtgttcaacg ggctcctgta	1351
	cgccggtggn gggcnccagt gnganggata tctgcagaat tcggctagcc gaattc	1407

FIGURE 42

5	tctagcgaac cccttcggac actgccagca tagacagcag cccctgctac tgtcccacca	60
	ctgtacccca gagccccgac tagcagt atg ccg gga gcg cca ggg cct ggg cct	114
	Met Pro Gly Ala Pro Gly Pro Gly Pro	
	1 5	
10	gag gtg gct gca gcc ttt gag gaa cgg ttg agt cag gca cta cag gaa	162
	Glu Val Ala Ala Ala Phe Glu Glu Arg Leu Ser Gln Ala Leu Gln Glu	
	10 15 20 25	
15	ctg cag gca gtg gct gaa gca ggc cgg tca gcg gtg acc cag gca gct	210
	Leu Gln Ala Val Ala Glu Ala Gly Arg Ser Ala Val Thr Gln Ala Ala	
	30 35 40	
20	gat gca gcc cta gcc act gta gag cca gtg gct cag gca tct gaa gag	258
	Asp Ala Ala Leu Ala Thr Val Glu Pro Val Ala Gln Ala Ser Glu Glu	
	45 50 55	
25	ctt cgg gcc gag aca gca gcc ctg agc cgg cgg ctg gat gcc ctg acc	306
	Leu Arg Ala Glu Thr Ala Ala Leu Ser Arg Arg Leu Asp Ala Leu Thr	
	60 65 70	
30	agg cag gtg gag gtg ctg agc cta cgg ctg ggt gtt cca ctc gtg ccg	354
	Arg Gln Val Glu Val Leu Ser Leu Arg Leu Gly Val Pro Leu Val Pro	
	75 80 85	
35	gac ctg gag tcc gag cta gag ccc agc gag ctg ttg ctg gct gct gcc	402
	Asp Leu Glu Ser Glu Leu Glu Pro Ser Glu Leu Leu Ala Ala Ala	
	90 95 100 105	
40	gac cct gag gcc ctc ttc cag gca agc tga ggatgctggg acccccgtgg	452
	Asp Pro Glu Ala Leu Phe Gln Ala Ser *	
	110	
45	ccacccgcct gccttttagca cccgccgcag ctcttctgcg ggccccctctc gaagcagcag	512
	tctcatggag cccgatccag cagagcccc ctctgccaca gtggaagcag ctaatggaac	572
	agagcagact ctggacaaag tgaacaaagg cccagagggg cggagcccc tgagtgcaga	632
	ggagctgatg gccattgagg acgaaggaat cctggacaag atgctggacc aggctacgaa	692
	ctttgaagag cggaagctca tccgggctgc gctccgtgag ctccgacaaa gaaagagaga	752
	ccagagggac aaggaacgag aacggcggct acgagaggca cggggccggc caggcgagag	812
	ccgaagcaat atggctacta cagagaccac caccaggcac aagccagagg gcggctgatg	872
	gctcggcggt cagcacagtt accaaaactg agcgggtcgt ccaactccaat gacggcacgc	932
	agactgcgcg caccaccaca gtggagtcga gtttcgtgag gcgctcggag aatggcagca	992
	gcaagcaagc agcagcacca cggctccaaac caagaccttt tcctcttctt ctctctcttc	1052
	caaaaaaatg ggcagtatct tcgaccgaga ggaccaaacc agctcacgtt ctggcagcct	1112
	ggcggccctc gaaaaacgcc aggcagagaa gaagaaagag ctcatgaagg cacagagtct	1172
	gcccagacc taagcgtccc aagcacgcaa ggcatgatt gagaaactag agaaggaagg	1232
	ctcttcgggc agtcttgga caccctgtac agcggtagac cgttctacca gcttcggagt	1292
	ccccaacgcc aacagcatca agcagatggt tctggactgg tgccgagcca agaccctgg	1352
	ctacgagcac gtggacatcc agaacttctc tccagctgga gtgatgggat ggctttctgt	1412
	gccctgtgac acaatttctt ccctgaggct tttgactatg gacagcttag cccacaaaac	1472
	ggcgccaga actttgaaat ggccttctca tctgctgaga cccatgcgga ctgccgcag	1532
	ctcctggata cagaggacat ggtgcggctt cgagagcctg actggaagtg cgtgtacacg	1592
	tacatccagg agttctaccg ctgtctggtc cagaaggggc tggtaaaaac caaaaagtcc	1652

FIGURE 43

5	tctagcgaac cccttcgctc cagggcgctt gcctcctgct gacttgctct tcaccattag	60
	acaagcctga cgtcaagacc cca atg gct aac gaa gct aac cct tgc cca tgt	113
	Met Ala Asn Glu Ala Asn Pro Cys Pro Cys	
	1 5 10	
10	gac att ggt cac agg cta gac tat ggt ggc atg ggc cag gaa gtt cag	161
	Asp Ile Gly His Arg Leu Asp Tyr Gly Gly Met Gly Gln Glu Val Gln	
	15 20 25	
	ggt gag cac atc aag gca tat gtc acc cgg tcc cct gtg gat gca ggc	209
15	Val Glu His Ile Lys Ala Tyr Val Thr Arg Ser Pro Val Asp Ala Gly	
	30 35 40	
	aaa gct gtg att gtt gtc cag gat ata ttt ggc tgg cag ctg tcc aac	257
	Lys Ala Val Ile Val Val Gln Asp Ile Phe Gly Trp Gln Leu Ser Asn	
20	45 50 55	
	acc agg tat atg gct gac atg att gct gga aat gga tac aca act att	305
	Thr Arg Tyr Met Ala Asp Met Ile Ala Gly Asn Gly Tyr Thr Thr Ile	
	60 65 70	
25	gcc cag act tct ttg tgg gtc aag agc cat ggg acc cgg ctg gtg att	353
	Ala Gln Thr Ser Leu Trp Val Lys Ser His Gly Thr Arg Leu Val Ile	
	75 80 85 90	
30	ggt cca cct tcc ctg agt ggt tga aatcaagaaa tgccagaaaa atcaaccgag	407
	Gly Pro Pro Ser Leu Ser Gly *	
	95	
	aggttgatgc tgtcttgagg tatctgaaac aacagtgtca tgcccagaag attggcattg	467
35	tgggcttctg ctgggggggt attgtggtgc accacgtgat gacgacatat ccagaagtca	527
	gagcgggggt gtctgtctat ggtatcatca gagattctga agatgtttat aatttgaaga	587
	acccaacggt gtttatcttt gcagaaaatg atgctgtgat tccacttgag caggtttcta	647
	tactgatcca gaagcttaaa gaacactgca tagttaatta ccaagttaag acattttctg	707
	ggcaaactca tggctttgtg catcggaaga gagaagactg ctcccctgca gacaaaccct	767
40	acattgagga agcgaggagg aatctcatcg aatggctgaa caagtatatt taacagcact	827
	caagcacaaa ttttgaataa ttaaattgac ccgaataatt aaattgaccc gaat	881

taaccctgc ttggggcccc acggatgctg gtggactgtg tacccttggt ggaggtggag 1712
gacatgatga tcatgggcaa aaagccagac cctaagtgcg tcttcaccta cgtgcaatcg 1772
FIGURE 42 (cont.)

5 ctgtacaacc acctgcggcg ccatgagctg cgcctgcgcg gcaagaatgt ctagccactg 1832
ctcacaccgc ctgcgctgca ggctgctgtc ccacgcccc aacaccggnc cctncagtgn 1892
gcctgccact gntgcccgtg tgtcgaaaca cctntcccct tgtcacacgc agngntttga 1952
taaattattt gntttnaaca aaaaaaaaaa aaaaaaaaaa aaaagcggcc gc 2004

10

15

20

25

30

35

40

45

50

55

12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

[illegible]

FIGURE 44 (CONT.)

Seq ID	CloneID	Kidney		Hyp 10w	Heart										
		PKD	Na + Ang2		LV						Spt				
					2w	4w	8w	12w	16w		2w	4w	8w	12w	16w
30	P00249_F09			—	▲	▲	▲	▲	▲		—	▲	—	▲	▲
31	P00258_A10			—	▲	▲	▲	▲	▲		—	—	—	—	—
32	P00262_C10			▲	—	▽	—	—	—		—	—	—	—	—
33	P00263_G06			▲	—	—	—	—	—		—	—	—	—	—
34	P00267_F08	—	—	▽	—	▲	—	▲	—		—	—	—	—	—
35	P00269_H08			▲	—	▽	—	▽	▽		—	—	—	—	—
36	P00312_C04				—	—	▽	—	—		—	—	▽	—	—
37	P00324_H02				—	▽	▽	▽	—		—	▽	▽	▽	▽
38	P00628_H02	▲	—	—	—	—	▲	▽	▽		—	—	—	—	—
39	P00629_C08			—	—	▽	—	—	▽		—	—	—	—	—
40	P00634_G11														
41	P00641_G11	—	—	▲	—	—	—	—	—		—	—	—	—	—
42	P00648_E12														
43	P00697_C03	▽	—	—	—	—	—	▽	▽		—	—	—	—	—